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version	- 2003
Core	c) 1993
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	Copyright

OM protein - protein search, using sw model

December 8, 2003, 09:13:30 ; Search time 22.0606 Seconds (without alignments) 179.063 Million cell updates/sec Run on:

US-09-498-556C-59 486 1 KATMQCGENEKYDSCGSKEC.....VSAEDCELDNMDFIYPGTRN 84 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues

Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	OB ID Description	1 CVP6 PIMHY OBtown oimple hypo	3 P56682	TUMAN 09v493	4OUSE 088799	RAT P98158	ASCSU P07851	AEEL 004833	Q28295	046202		P07852		P98155		P35953	P98166		1 ITRI ASCSU P19398 ascaris suu	CHICK P10039	Q9tui5	Q9ukf2 homo	P04275 homo	UMAN P35555 homo	Q9tv36 sus s	NISI 077417	1 ITB1_XENLA P12606 xenopus lae	VIN P80012	1 UNSZ CAEEL 006561 caenorhabdi	MOUSE P27512	CAEEL P41950	1 HMCT BOMMO P98092 bombyx mori	1 VSM5_TRYBB P26333 trypanosoma
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de	Query Match	24.1	22.7	21.2	20.6	19.4	19.0	19.0	•	٠	•	17.6	٠	•	٠	٠	17.0	•	16.9	•	٠	16.5	16.4	16.4	٠		•	•	16.2	16.0	16.0	16.0	15.9
	Score	117	110.5	103	100	94.5	92.5	92.5	87.5	87	86.5	85.5	85.5	82.5	82.5		82.5	82.5	82	81.5	81		79.5	79.5	79.5	78.5	78.5	78.5	78.5	78	78	78	77.5
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Q61554 mus musculu P47944 homo sapien P47945 mus musculu P09055 mus musculu P01049 ascaris suu P98163 drosophila P10040 drosophila P10040 drosophila P49134 rattus norv O77416 anisakis si Q05439 plasmodium Q62919 rattus norv P22105 homo sapien	
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FBN1 MOUSE MT4 HUMAN MT4 MOUSE ITR2 ASCSU ITR2 ASCSU ITR2 ASCSU ITR2 BROME ITR1 BAT ASP1 ANISI OS28 PLAGA NEL1 RAT TENX_HUMAN	
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2871 62 62 798 1984 2139 779 779 2222 810	
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77.5 77 77 76.5 76.5 76.5 76.5 75.5 75.5	
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ALIGNMENTS

24.1%; Score 117; DB 1;	24.1%; Score 117;
DB 1;	24.1%; Score 117; DB 1; Similarity 35.4%; Pred. No. 4.1e-05;

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                                                                                                                                                                                                                                                                                                                                                                                                         Bania J., Stachowiak D., Polanowski A.;
"Primary structure and properties of the cathepsin G/chymotrypsin inhibitor from the larval hemolymph of Apis mellifera.";
Eur. J. Biochem. 262:680-687(1999)
-!- FUNCTION: Chymotrypsin and cathepsin G inhibitor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
PDB; 1CCV; 12-MAR-99.
InterPro; 1PR002919; TIL_CYsrich.
PFam; PF01826; TIL; 1.
                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZAN HUMAN STANDARD; PRT; 2812 AA.
Q9Y493; Q00218; Q96LB5; Q96LB6; Q96LB7; Q96LB9; Q96LB9; Q9BXN9; Q9BXN9; Q9BZ86; Q9BZ86; Q9BZ87; Q9BZ88; Q9BZ88; Q9BZ87; Q9BZ88; Q9BZ8, Q9BZ88; Q9BZ88; Q9BZ8, Q9BZ88; Q9BZ8, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.7%; Score 110.5; DB 1; Length 56; 33.3%; Pred. No. 0.00013; ive 8; Mismatches 25; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5973 MW; 092B2815AE6B2B7F CRC64;
                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SPE-2003 (Rel. 42, Last annotation update)
Chymotrypsin inhibitor (AMCI).
                        56 AA
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                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99339935; PubMed=10411628;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND STRUCTURE BY NMR
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                           STANDARD;
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Homo sapiens (Human).
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nes 22; Conserv
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=7460;
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116
20
38
38
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                        APIME
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SEQUENCE
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P56682;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOWALN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHAUS.
-!- DOMAIN: The WWFD domain 2 may mediate covalent oligomerization (by
similarity to human intestinal mucin MUC2).
-!- SIMILARITY: Contains 3 MAM domains.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- CAUTION: Ref. 2 sequence differs from that shown due to
transposition of a number of exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I. FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
                                                                                                                                  PARTIAL SEQUENCE FROM N.A. MEDLINE=99018118; PubMed=9799793; Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui L.-C., Rosenthal A.; Rosenthal A.; analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci reveals 17 genes.";
                                                                                                                                                                                                                                                                                                                                          MEDLINE=21138439; PubMed=11239002; Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.; Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN)."; zonadhesin gene (ZAN).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=Q9Y493-7; Sequence=VSP 001426, VSP 001427; TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS. DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
                                                   Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.; "Multiple intra-species variants of human zonadhesin."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9Y493-4; Sequence=VSP_001424, VSP_001425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9Y493-3; Sequence=VSP_001428, VSP_001429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9Y493-5; Sequence=VSP_001420, VSP_001421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9Y493-2; Sequence=VSP_001430, VSP_001431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9Y493-6; Sequence=VSP_001422, VSP_001423;
            FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1810-2812 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2375-2683 FROM N.A. (ISOFORM 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9Y493-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                                                                                                                  Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZONA PELLUCIDA.
                                      TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=3
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N-LINKED (GLCNAC) (POTENTIAL). HGVSS WAAAF (in isoform 5).	/rincrostroiser. Missing (in lasform 5). /FTid=VSP 001421.	HGVSSRYHISELYDTLPSILC -> YAILCQEAGAALAGWR DRTLC (in isoform 6).	/FIIG=VSF U01422. Missing (in isoform 6).	/FILG=VSF UL423. HGVSRYHISELYPTLEPSILCQPGRPRG -> YALLCQEAG	/FILENCE AND	FIRESTING (IN 180101111 4). /FILESTED (141455. HOUGGENERT FOR FORT FORT FORT FORT	novasatinishiii ilesiiloyeenka marka	/FTId=VSP_001426. LGSS -> VRAGSRRPWGAEAPRRARPGMELERLLLALPFL	AGQQ (in isoform 7). /FTId=VSP 001427.	HGVSSRYHI <u>S</u> ELYDTLPSILCQPGRPRGLRGPLRGRLRQHP RLCLQWHPEPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC	ASSRILLCEPF -> YAILCQEAGAALAGWRDRTLCAMECP AGTIYQSCMTPCPASCANLADPGDCEGPCVEGCASIPGYAY		/FTId=VSP 001428. Missing (In isoform 2).	/FIId=VSP_001429.	RECEQMHPEPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC	ASSRILLCEPFSCRAGEVCTLGNHTQGCFPESPCLQNPCQN DGQCR -> YAILCQEAGAALAGWRDRTLCAMECPAGTIYQ	SCMTPCPASCANLADPGDCEGPCVEGCASIPGYAYSGTQSI	SWPFPFLAGOOLSD (in isoform 1).	/FTId=VSP 001430. Missing (In isoform 1).	$/FTIG=VSP_001431$. H -> Q ($I\overline{IN}$ REF. 1; AAK01431/AAK01432/		Score 103; UB 1; Length 2812; Pred, No. 0.033;	10; Mismarches 30; indels 16; Gaps 5;	ATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEGGFYRNKD 61	CPASCKSPRPSC-GPLCREGCVCNPGFLFS-D 1084	FIYPG 81	: YYEPG 1105			PRT; 5376 AA.	(heated)	section undate)			tta; Craniata; Vertebrata; Buteleostomi; :ia; Sciurognathi; Muridae; Murinae; Mus.		
2701 2601	2812	2617	2708	2624		2107	9 7 9 7	2666		2689			2812	27.74	#7/7				2812	430		Z1.28; y 30.98;	conservative	EKYDSCGS!	STERCPPNARYESCACPASCK-	DKCVSAEDCE-LDNMDFIYPG	1085 NHCIQASSCNCFYNNDYYEPG			STANDARD;				se).	a; Chorda a; Rodent		SEQUENCE FROM N.A. TISSUE=Testis; MEDLINE=98123114; PubMed=9452463;
2701 2597	2602	2597	2618	2597	3636	25020	607	2663		2597			2690	2597	1607				2725	430		.5		ATMOCGEN	STERCPPN	DKCVSAED	: : NHCIQASS			ST	08647; 01 (Rel	01 (Rel. 40,	precur	lus (Mouse)	; Metazo Eutheri	, , , , , , , ,	FROM N.A stis; 8123114;
CARBOHYD	VARSPLIC	VARSPLIC	VARSPLIC	VARSPLIC	UND GOT IC	VAPODITO	Andreas and	VARSPLIC		VARSPLIC			VARSPLIC	VAPCD1.TO	VARSFULL				VARSPLIC	CONFLICT	40.40	Dest Local S	cues 25;	6	1040	62	1085		RESULT 4	ZAN MOUSE	O88799; O08647; 16-OCT-2001 (Rel 40)	16-0CT-2001	Zonadhesin precursor.	Mus musculus	Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCDT mathalogo.	[1]	SEQUENCE FROM N.A. TISSUE=Testis; MEDLINE=98123114;
announce/							•												-			••												10.1			
(See http://www.isb-sib.ch/an)									ne, NAS. zona pellucida; NAS.												_	a dule		SNTIAL).	TIAL) .		66 X HEPTAPEPTIDE REPEATS (APPROXIMATE)	•							.) (POTENTIAL)) (POTENTIAL).		.) (POTENTIAL). .) (POTENTIAL). .) (POTENTIAL).
agreement @isb-sib.ch	1,	11:				1; 1: ALT SEO.	' ;		plasma memorane; NAS. of sperm to zona pell	cognition; NAS. 11 adhesion; NAS.	InterPro; 1PR006209; BGF 11Ke. InterPro; IPR000999; Max domain.	Cysrich.	ນ່ ດ								3. namombrano. DCD-14ko d	ing. potental.	ZONADHESIN.	EXTRACELLULAR (POTENTIAL) POTENTIAL.	CYTOPLASMIC (POTENTIAL)		66 X HEPTAPEPTIDE	(MUCIN-LIKE DOMAIN) VWFD 1.	VWFD 2.	VWED 4.	EGF-LIKE. BY SIMILARITY.	BY SIMILARITY. BY SIMILARITY.	N-LINKED (GLCNAC.	N-LINKED (GLCNAC.	N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED)	N-LINKED (GLCNAC.	N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED)
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s requires an email t	F332975;	AF332977; AF332978; AF332979;	F332980;	Y046055; Y046055;	Y046055;	X046055; F053356;	AF312032; U83191; AA	7; HGNC:1285 602372;	0007339;	0008037; 0016337;	0; 1PR000 0; 1PR000	o; IPR003	o; IPR001 5; IPR001	F00629; N F01826; T	F02345, T	F00094; V SM00181;	SM00137; SM00214;	SM00215;	PS00022	PS01186	; PS50060	Alternat	18	18 M 2758	2779	209	573	1156	1542	2331							2542
entities or send		EMBL; Al	EMBL; A	EMBL; A	EMBL; A	EMBL; A	EMBL; A	Genew; MIM; 60;	38	66 66 66 67 68 68 68 68 68 68 68 68 68 68 68 68 68	InterPr	InterPr	InterPr	Pram; P	Pfam, P	SMART;	SMART; S	SMART:	PROSITE,	PROSITE,	PROSITE	Repeat;	CHAIN	DOMAIN TRANSMEM	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DISULFID	DISULPID	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD CARBOHYD
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3412 KITLQCPAHTQYTSC-LPSCLPSC----LDPEGLCKDISPKVP---STCKEGCVCQSGYV 3463
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      80 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).
VWFD 1 (PARTIAL).
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                                                                                                                                                                                                                               -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBUNIT: PROBABLY FORMY HEAD.
-!- TISSUE RECIPION OF THE SPERM HEAD.
-!- TISSUE SPECIFICITY: IN TESTIES, PRIMARILY IN HAPLOID SPERMATIDS.
-!- DOMAIN: THE WAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
-!- DOMAIN: UNING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE WUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOUTING ADHESION TO THE OUTCOTAL ISTHMUS.
-!- DOMAIN: THE VWFD DOMAIN ADHESION TO THE OUTCOTAL ISTHMUS.
-!- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- SIMILARITY: CONTAINS 3 MAM domains.
-!- SIMILARITY: CONTAINS 1 EGF-like domain.
                                                                                                                                                             zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01186; EGF_2; 18.
PROSITE; PS00740; MAM 1; FALSE_NEG.
PROSITE; PS50060; MAM 2; FALSE_NEG.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                   TISSUE=Testis;
MEDLINE=97271566; PubMed=9126492;
Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zonadhesin gene and the human
               "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
MAM 1.
MAM 2.
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EMBL; U33190; AAC53125.1; --
PIR; T42221; T42215.
MGJ; MGJ; MGI:106656; Zan.
InterPro; IPR0036209; EGF like.
InterPro; IPR0036210; IEGF.
InterPro; IPR00399; MAM domain.
InterPro; IPR00399; MAM domain.
InterPro; IPR00399; TIL Cysrich.
InterPro; IPR00399; TIL Cysrich.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
Fam; PF00245; TIL; 25.
Ffam; PF00245; TIL; 25.
Ffam; PF00246; TIL; 25.
Ffam; PF00246; VWd; 4.
SWART; SW00131; MAM; 2.
SWART; SW00131; MAM; 2.
SWART; SW00214; VWC; 17.
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PROSITE; PS0186; EGF2; 18.
PROSITE; PS00740; MAM—1; FALSE_NEG.
PROSITE; PS50060; MAM—2; 3.
                                                        Biol. Chem. 273:3415-3421(1998)
                                                                                       SEQUENCE OF 4864-5376 FROM N.A.
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   Sao Z., Garbers D.L.;
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LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
HSSP; Q07954; 1CR8.

BR (1970SuiteDB); P98158; -.

GlycoSuiteDB); P98158; -.

BR (1970SuiteDB); P98158; -.

BR (1970SuiteDB); P98158; -.

BR (1970SuiteDB); P98158; -.

BR (1970SuiteDB); P88158; GRC Ca.

BR (1970SuiteDB); BGF (1970SuiteDB); BGF (1970SuiteDB); BGF (1970SuiteDB); BGF; 13.

BR (1970SuiteDB); BGF; 13.

BR (1970SuiteDB); BGF (1970SuiteDB); BG
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LDL-RECEPTOR CLASS B 12.
LDL-RECEPTOR CLASS B 12.
LDL-RECEPTOR CLASS B 13.
LDL-RECEPTOR CLASS B 14.
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CYTOPLASMIC (POTENTIAL)
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LDL-RECEPTOR CLASS A 2
LDL-RECEPTOR CLASS A 3
LDL-RECEPTOR CLASS A 4
LDL-RECEPTOR CLASS A 5
LDL-RECEPTOR CLASS A 6
LDL-RECEPTOR CLASS A 7
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LDL-RECREPTOR CLASS B
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
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LDL-RECEPTOR CLASS A LDL-RECEPTOR CLASS A
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LDL-RECEPTOR CLDL-RECEPTOR CLD-RECEPTOR CLD-
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EGF-LIKE 2.
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                  MEDLINE=94172242; PubMed=7510321;
MEDLINE=94172242; PubMed=7510321;
A Zheng G., Bachinaky D.R., Stamenkovic I., Strickland D.K., Brown D.,
A Andres G., McCluskey R.T.;
"Organ distribution in rats of two members of the low-density
Ilpoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
receptor-associated protein (RAP).";
I. Histochem. Cytochem. 42:531-542(1994).
II. J. Histochem. Cytochem. 42:531-542(1994).
II. J. HISTOCHEM ACTIVATOR PLASMINOGEN ACTIVATOR INHIBITOR TYPE I
COMPLEX, APOLIPOPROTERIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
IACTOFERRIN, CLUSTERIN AND CALCIUM.
COMPLEX, APOLIPOPROTERIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
IACTOFERRIN, CLUSTERIN AND CALCIUM.
APROTININ, ANINOGLYCOSIDES AND POLYMAKIN B.
C. I- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS
APROTININ, ANINOGLYCOSIDES AND POLYMATIN B.
C. I- SUBGINIT: Forms a multimeric complex together with a receptor-
associated protein (RAP). Binds to ankyrin-repeat family A protein
C. I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXPRESSED IN
CLEAVARGA AT THE CELL SURFACE.
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                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330) (gp330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95386696; PubMed=7544804;
Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,
Noris K., Gliemann J., Christensen E.I.;
"Evidence that epithelial glycoprotein 330/megalin mediates uptake of
polybasic drugs.";
J., Clin. Invest. 96:1404-1413(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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-i- SIMILARITY: Contains 34 LDL-receptor class A domains.
-i- SIMILARITY: Contains 37 LDL-receptor class B domains.
-i- SIMILARITY: Contains 17 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G., "Complete cloning and sequencing of rat gp330/'megalin,' a distinctive member of the low density lipoprotein receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
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STRAIN=Sprague-Dawley; TISSUE-Kidney;
MEDLINE=95024033; PubMed=7937880;
                                                                         3464 LN-SDKCVLRAECD 3476
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                  P07951; 077419; 01. Created) 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Chymorrypain/elastase isoinhibitor I (C/E-1 inhibitor) (AsC/E-1). Ascaris suum (Pigr roundworm) (Ascaris lumbricoides) Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDDLINE-98297373; PubMed=9635450;
Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
Lu R.C., mutational bursts in the reactive site centers of serine protease inhibitors from an ascarid nematode.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95006335; PubMed-7922044; Manang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.; "The molecular structure of the complex of Ascaris chymotrypsin/elastase inhibitor with porcine elastase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structure 2:679-689[1994].
-!- FUNCTION: Defend the organism against the host's proteinases.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
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                                                                                                                                                                                                                                                                                                                                    MEDLINE=84255715; PubMed=6564898;
Babin D.R., Peanasky R.J., Goos S.M.;
"The isoinhibitors of chymctrypsin/elastase from Ascaris
lumbricoides: the primary structure.";
Arch. Biochem. Biophys. 232:143-161(1984).
314 LNCEYQCHQTPFGGECFCPPGHIINSNDSRTCIDFDDCQI 353
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PD -> DP (IN REF. 2)
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PDB, LEAT, 05-APR-99.
InterPro; IPR002919; TIL_Cyerich.
Pfam; PP01826; TIL; 1.
Serine protease inhibitor; 3D-structure.
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                                                                                                  STANDARD;
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NCBI_TaxID=6253;
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LDL-RECEPTOR CLASS A 33.
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LDL-RECEPTOR CLASS A 35.
LDL-RECEPTOR CLASS A 35.
LDL-RECEPTOR CLASS A 36.
EGF-LIKE 15,
CLDL-RECEPTOR CLASS B 35.
LDL-RECEPTOR CLASS B 35.
LDL-RECEPTOR CLASS B 36.
EGF-LIKE 16,
CALCIUM-BINDING (POTENTIAL).
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                63
                                                                                              53
                                                                             6 CGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCE--EGFYRNKDDK
                                                                                       SEQUENCE FROM N.A.

MEDLINE=93281621; PubMed=8506301;
Yochem J., Greenwald I.;

"A gene for a low density lipoprotein receptor-related protein in the nematode Caenorhabditis elegans.";

Proc. Natl. Acad. Sci. U.S.A. 90:4572-4576(1993).
                                                               13; Gaps
                                                                                                                                                                                                                                 Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                         004833;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Low-density lipoprotein receptor-related protein precursor (LRP).
LRP-1 OR F29D11.1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                      Wilkinson J.;
Submitted (WAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (WAY-1996) to the EMBL/GenBank/DDBJ databases.
SUBMITTED WAY ACT AS A RECEPTOR FOR THE ENDOCTYOSIS OF
EXTRACELLULAR LIGANDS SUCH AS CHYLOMCRON REMNANTS, PROTEASE-
INHIBITOR COMPLEXES AND VITELLOGENIN.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SIMILARITY: Contains 35 LDL-receptor class A domains.
--- SIMILARITY: Contains 17 EGF-like domains.
                                              Score 92.5; DB 1; Length 63;
Pred. No. 0.0076;
5; Mismatches 27; Indels 1
                               5DC10DE75B375F16 CRC64;
                                                                                                                                                                     PRT; 4753 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Ask hydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001891; EGF_Ca.
InterPro; IPR002172; LDL receptor_A.
InterPro; IPR000313; Ldl_receptor_A.
InterPro; IPR00033; Ldl_receptor_rep.
Pfam; PP00058; Idl_recept_a; 34.
Pfam; PP00058; Idl_recept_b; 26.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00179; EGF_CA; 2.
                                            19.0%;
32.8%;
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                               6862 MW;
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HSSP; Q07954; ICR8.
WormPep; F29D11.1; CE05765.
                                                     Local Similarity 32.8
ses 22, Conservative
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                                                                                                                            54 CIPASOC 60
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                               63 AA;
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-:- TISSUE SPECIFICY: BLOOD.
-:- PTH: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
-:- SIMILARITY: Contains 3 VWFA domains.
-:- SIMILARITY: Contains 3 VWFC domains.
-:- SIMILARITY: Contains 1 VWFC domains.
-:- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
-:- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
                                                                                                                                   7 GENEKYDSCGSKEC-------DKKCKYDGVEEDDEEPNVPC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D., "Complete sequence of the structural gene for canine von Willebrand factor and identification of a mutation causing Scottish terrier von Willebrand's disease.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                             41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Blood;
Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
Mancuso D.J., Christopherson P.A., Kroner Bequence and expression of
a region encoding the glycoprotein Ib/IX binding domain.";
Submitted (JAN-1994) to the EMBL/GenBank/DBBJ databases.
-!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
VASCULAR INJURY (BY SIMILARITY).
-!- SUBUNIT: MULTHMERIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibuya H., Nonneman D.J., Holzhauer J., Mohammed I.H.,
                                                                                                                                                                                                                                  1233 FRCANGRQCVPLRNHCDGQSDCEDG---SDEDSCAVTAESCTPDQFKCVSSG 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
                                                                                                                                                                                                               81
                                                                                                                                                                                                               -----LVRVCHQDCVCEEGFYRNKDDKC-VSAEDCELDNMDFIYPG
                                                     Length 4753;
                                                                                             Indels
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Montgomery R.R., Fahs S., Montgomery M.W.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Johnson G.S.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                           32;
                                                     ; Score 92.5; DB 1;
; Pred. No. 0.57;
11; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                            ONE 20295, 028311, 0297S14;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
VWF OR FBVWF.
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25.0%;
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Best Local Similarity 25.0°
Matches 28, Conservative
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STRAIN=Canton-S; TISSUE=Male accessory gland;
MEDLINE=99135120; PubMed=9474779;
Wolfner M.F., Harada H.A., Bubam M.J., Stelick T.J., Kraus K.W.,
Kalb J.M., Lung Y.O., Neubaum D.M., Park M., Tram U.K.;
"New genes for male accessory gland proteins in Drosophila
                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.0%; Score 87.5; DB 1; Length 2813; 28.4%; Pred. No. 1; tive 9; Mismatches 30; Indels 9
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 309716 MW; 5DF93E1E5E72F80C CRC64;
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V -> I (IN REF. 3).
A -> G (IN REF. 2).
I -> V (IN REF. 2).
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TO G46202;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2003 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT Accessory gland protein Acp62F precursor.

GN ACP62F OR CG1262.
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Insect Biochem. Mol. Biol. 27:825-834(1997)
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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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EMBL; U66246; AAB93766.1; -.
HSSP; P04275; 1AUQ.
InterPro; IPR006208; Cys_knot.
InterPro; IPR006209; Cys_knot.
InterPro; IPR000004; SapB.
InterPro; IPR0010019; TIL_Cysrich.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gutton G.G., Worthand J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Feleffer B.D., RA Handon R.C., Batter E.G., Helt G., Champpe M., Feleffer B.D., RA Ballew R.M., Basu A., Barchalal J., Bayraktarolu L., Beasley E.M., Beson K.Y., Benos P.V., Barman B.P., Bhandari D., Bolshakov S., Buttlar R.M., Bauu A., Bautler H., Cadieu E., Center A., Chadra I., Rokva D., Buttler H., Cadieu E., Center A., Chadra I., Raburis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Buttls R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Buttls R.C., Busam D.A., Dahlke C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P. Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P., Adoler R., Gong F., Gorrell J.H., Gu Z., Genbart M.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A., Hostin D., Houston K.A., Hallan T.J., Harris M.L., Harris M.L., Harvey P. Heimand T.J., Harris M.L., Mcalush F., Karpen G.H., Kez J., Karlis D. Lai Z., Liang Y., Lin X., Manlel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Manlel B.E., Kallishian M.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Mushin M.Y., Mobarry C., Morris J., Moshrefi A., Mount S.M., Molson D., Mulliams S.M., Modager T., Worlas R., Shen H., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Sant H., Spier E., Saradling A.C., Stapleton M., Stupski M., P., Sant H., Wallen S.M., Woodege T., Walsen M., Woodes M., Woodes M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics 156:1879-1888(2000).
-!- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN MATED FEMALE FLIES. MAY CONTRIBUTE TO THE TOXICITY OF SEMINAL FLUID AND THE DECREASED LIFE-SPAN OF MATED FEMALES. MAY ALSO AFFECT NEUROMUSCULAR EVENTS AFFER MATING CONCERNING SPERM STORAGE
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STRAIN=ZIM62H-12C, ZIM62H-16C, ZIM62H-28C, ZIM62H-30C, ZIM62H-34C,
STRAIN=ZIM62H-10C, ZIM62H-11C, ZIM62I-18C, and ZIM62I-53C;
ZIM62I-SC, ZIM62I-10C, ZIM62I-1131;
MEDLINE=Z055613; Pubmed=11101381;
Begun D.J., Whitley P., Todd B.L., Waldrip-Dail H.M., Clark A.G.;
"Molecular population genetics of male accessory gland proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted (Probable).
TISSUE SPECIFICITY: SEMINAL FLUID.
SIMILARITY: SOME, TO P.NIGRIVENTER TX2-6.
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TISSUES-Kidney,
TISSUES-Kidney,
MEDLINE-96306376; PubWed=8706697;
Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I.,
BK B., Larsson M., Juhlin C., Hellman P., Davis H., Aekerstroem G.,
Rask L., Morse B.;
"Cloning and sequencing of human gp330, a Ca(2+)-binding receptor
                                                                                                                                                                                                                                                                                 4 MQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRN-KDD
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MEDLINE-94244704; PubMed=8187828;
Lundgren S., Hjaelm G., Hellman P., Ek B., Juhlin C., Rastad J.,
Klareskog L., Aakerstrom G., Rask L.;
"A protein involved in calcium sensing of the human parathyroid and
placental cytotrophoblast cells belongs to the LDL-receptor protein
superfamily.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  POTENTIAL.
ACCESSORY GLAND PROTEIN ACP62F.
                                                                                                                                                                                                                  17.9%; Score 87; DB 1; Length 115; 31.0%; Pred. No. 0.047; tive 8; Mismatches 29; Indel8
                                                                 GO, GO:0004867, F:serine protease inhibitor activity, IDA.
InterPro, IPR002919, TIL_Cysrich.
Pfam, PF01826, TIL, 1.
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   4326AA6F6C32291D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with potential intracellular signaling properties.";
Eur. J. Biochem. 239:132-137(1996).
                                                                                                                                                                                                                               31.0%; Prec. ...
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EMBL, AX010615, AAG35374.1; -. EMBL, AX010616, AAG35375.1; -. EMBL, AX010617, AAG35376.1; -. FlyBase, FBGN0020509, Acp62F.
                                                                                                                                                                                   115 AA; 12570 MW;
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                                                                                                                                                                                                                               Local Similarity 31.0 tes 22; Conservative
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| LDL-RECEPTOR CLASS A 5. |
| LDL-RECEPTOR CLASS A 7. |
| EGF-LIKE 2. |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R MAM; 600013; -.

R GO; GO:0005564; C:1ysosome; TAS.

GO; GO:0006689; P:1pid metabolism; TAS.

R GO; GO:0006898; P:protein amino acid glycosylation; TAS.

R GO; GO:0006898; P:receptor mediated endocytosis; TAS.

R InterPro; IPR000152; Asx hydroxyl.

R InterPro; IPR000152; Asx hydroxyl.

R InterPro; IPR000172; Like.

R InterPro; IPR000173; Ldl_receptor_A.

R Pfam; PF00007; Idl_receptor_rep.

R Pfam; PF00007; Idl_receptor_rep.

R Pfam; PF00057; Idl_recept_a; 36.

R Pfam; PF00057; Ldl_a; 36.

R PRART; SM00179; EGF_CA; 3.

R RNART; SM00135; LbLa; 36.

R PROSITE; PS00106; ASX HYDROXYL; 4.

R PROSITE; PS01186; EGF_2; 9.

R PROSITE; PS01186; EGF_2; 9.

R PROSITE; PS01186; EGF_2; 9.

R PROSITE; PS0109; LDLRA 1; 31.

R ROSITE; PS0109; LDLRA 2; 36.

R GJYCOPROTEDING GOMAIN; Signal; SH3-binding; Polymorphism.

T SIGNAL

T CHAIN DEVENTIAL, INDEMENDED PER PERFORMATIAL, LEDER PERFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pits; Transmembrane;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
LDL-RECEPTOR CLASS A 1.
Exp. Cell Res. 212:344-350(1994).
[5]
                                                                       MEDLINE=95286588; PubMed=7768901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U33837, AAB41649.1, -...
EMBL, U04441, AAB02882.1, -...
EMBL, S73145, AAB30825.1, -...
PIR, IS3413, I53413.
HSSP, Q07954, ICR8.
Genew, HGNC:6694, IRP2.
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TRANSMEM
DOMAIN
DOMAIN
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SKELETAL MUSCLE
  53 CVPVSEC 59
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                                                                                                                                                                                             NCBI_TaxID=9031;
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                                                         CHICK
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                                                                                                                                                             6 CGENEKYDSCGSKEC-----DKKC-----KYDGVEEEDDEEPNVPCLVRVCHQD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCE--EGFYRNKDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Chymotrypain/elastase isoinhibitors 2 to 5.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Babin D.R., Peanasky R.J., Goos S.M.;
The isoinhibitors of chymotrypain/elastase from Ascaris
lumbricoides: the primary structure.";
Arch. Biochem. Biophys. 232:143-161(1984).
-1- FUNCTION: Defend the organism against the host's proteinases.
-1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
InterPro; IPRO02919; TIL_Cysrich.
Pfam; PF01826; TIL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.037;
ches 28; Indels 13;
                                                                                                                                      21;
                                                                                                                 DB 1; Length 4655;
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                                                                                                                                      30; Indels
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CLASS A 28.
CLASS A 30.
CLASS A 31.
CLASS A 31.
CLASS A 33.
CLASS A 34.
CLASS A 35.
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                                                                                                                          2.1;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                         65 AA
LDL-RECEPTOR C
                                                                                                                 ; Score 86.5; [; Pred. No. 2.1; 14; Mismatches
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                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
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DOMAIN 4 59
DISULFID 4 37
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nes 19; Conservative
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3795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 510-518; 546-554 AND 819-827.

STRAIN=White leghorn; TISSUE=Follicle membrane;

MEDLINE=92011638; PubMed=1655760;

MEDLINE=92011638; PubMed=1655760;

MEDLINE=92011638; PubMed=1655760;

The receptor for yolk lipoprotein deposition in the chicken oocyte.";

J. Biol. Chem. 266:18761-18770(1991).

-! FUNCTION: Binds VLDL and transports it into cells by endocytosis.

-! FUNCTION: Binds VLDL and transports it into cells by endocytosis.

In order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits. Binding to Reelin induces tyrosine phosphorylation of Dabl and modulation of Tau
                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                               STRAIN=White leghorn; TISSUE=Ovary;
MEDLINE=595045409; PubMed=7957081;
MEDLINE=595045409; PubMed=7957081;
Bujo H., Hermann M., Kaderli M.O., Jacobsen L., Sugawara S.,
Nimpf J., Yamamoto T., Schneider W.J.;
"Chicken occyte growth is mediated by an eight ligand binding repeat
member of the LDL receptor family.";
EMBO J. 13:5165-5175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEART AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Binds to the extracellular matrix protein Reelin (By
                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 31, Last sequence update)
028-FRB-2003 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor (VLDL receptor)
(Vitellogenin receptor) (VTG receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULÂR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: ABUNDANT IN OOCYTES; MUCH LESS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 8 LDL-receptor class A domains. -!- SIMILARITY: Contains 6 LDL-receptor class B domains. -!- SIMILARITY: Contains 3 EGF-like domains.
  863 AA.
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InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0010181; EGF_Ca.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000313; Ldl_receptor_rep.
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  PRT;
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Pfam; PF00005; 1dl recept a; 8.
Pfam; PF00058; 1dl recept b; 5.
PRINTS; PR00261; LDLRECEPTOR.
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SMART; SM00179; EGF CA; 2.
SMART; SM00192; LDLa; 8.
SMART; SM00135; LY; 5.
STANDARD;
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LDLa; b.
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255 VKCSTSEV--QCGSGECIHKKWRCDGDPDCKDGSDEINCPSRTCRPDQFRCEDGNCIHGS

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(POTENTIAL)
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VERY LOW-DENSITY LIPOPROTEIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 8.
EGF-LIKE 2, CALCIUM-BINDING (POTER LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 5.
LDL-RECEPTOR CLASS B 5.
LDL-RECEPTOR CLASS B 6.
EGF-LIKE 3.
RSTENICARITY.
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BY
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PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS01209; LDIMA,1; 8.
PROSITE; PS50666; LDIMA,2; 8.
Glycoprotein; VLDL; Cholesterol metabolism; Lipid transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85.5; DB 1; Length 863; Pred. No. 0.49;
                                                                              pits; Transmembrane; Receptor; Signal;
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                                                           Glycoprotein; VLDL; Chol
Endocytosis; Coated pits
EGF-like domain; Repeat.
SIGNAL
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863 AA;
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Best Local Similarity
Matches 25; Conserv
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lipoprotein/apolipoprotein E receptor and assignment of the gene chromosome 9pter-p23."; Somat. Cell Mol. Genet. 19:557-569(1993).

TISSUE=Skeletal muscle; MEDLINE=94174378; PubMed=8128315; Gafvels M.E., Caird M., Britt D., Jackson C.L., Patterson D., Strauss J.F.; 'Cloning of a cDNA encoding a putative human very low density

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human)

VLDLR.

SEQUENCE FROM N.A. NCBI_TaxID=9606;

01-07T-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Very low-density lipoprotein receptor precursor (VLDL receptor)

873 AA

PRT;

STANDARD;

HUMAN

LDVR HUMAN

P98155

Webb J.C., Patel D.D., Jones M.D., Knight B.L., Soutar A.K.; "Characterization and tissue-specific expression of the human 'very low density lipoprotein (VLDL) receptor' mRNA."; Hum. Mol. Genet. 3:531-537(1994).

MEDLINE=94348496; PubMed=8069294;

SEQUENCE FROM N.A.

TISSUE=Heart

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"Characterization of single-nucleotide polymorphisms in coding regions
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SEQUENCE FROM N.A.
MEDLINE-94124575; PubMed-8294473;
Sakai J., Hoshino A., Takahashi S., Miura Y., Ishii H., Suzuki H.,
Kawarabayasi Y., Yamamoto T.;
"Structure, chromosome location, and expression of the human very low
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MEDLINE=99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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Nat. Genet. 23:373-373(1999).
-!- FUNCTION: Binds VLDL and transports it into cells by endocytosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            density lipoprotein receptor gene."; J. Biol. Chem. 269:2173-2182(1994).
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Nat. Genet. 22:231-238(1999).
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DDT TO DD
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4 61

Gaps

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36; Indels

Pred. No. 0.49; 9; Mismatches

25; Conservative

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                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
In order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits. Binding to Reelin induces tyrosine phosphorylation of Dabi and modulation of Tau phosphorylation (By similarity). SUBUNIT: Binds to the extracellular matrix protein Reelin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO: 0005041; F:low-density lipoprotein receptor activity; TAS.
R GO; GO: 0005613; P:memory; TAS.
R GO; GO: 0007613; P:memory; TAS.
R GO; GO: 0007613; P:memory; TAS.
R GO; GO: 0007165; P:signarcagenesis; TAS.
R InterPro; IPR000152; Asx hydroxyl.
R InterPro; IPR000152; Asx hydroxyl.
R InterPro; IPR00151; EQF_Ca.
R InterPro; IPR00151; EQF_Ca.
R InterPro; IPR00151; Ldl_receptor_rep.
R InterPro; IPR000033; Ldl_receptor_rep.
R Pfam; Pr000057; Idl_recept_a; 8.
R Pfam; Pr00056; Idl_recept_b; 5.
R RNART; SM00199; EGF_Ca; 2.
R SMART; SM00199; EGF_CA; 2.
R SMART; SM00195; LDLa; 8.
                                                                                                                                                                                      IBOId=P98155-2; Sequence=VSP 004304;
TISSUE SPECIFICITY: ABUNDANT IN HEART AND SKELETAL MUSCLE; ALSO OVARY AND KIDNEY; NOT IN LIVER.
SIMILARITY: Contains 8 LDL-receptor class A domains.
SIMILARITY: Contains 6 LDL-receptor class B domains.
SIMILARITY: Contains 3 EGF-like domains.
                                                                            similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
ALTERNATIVE SPLICING; Named isoforms=2;
Name=Long;
Isoid=P98155-1; Sequence=Displayed;
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BAA03969.1;
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PIR; A49729; A49729.
HSSP; PO1130; 1AJJ.
Genew; HGNC:12698; VLDLR.
MIM; 192977;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L20470; AAA53684.1;
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BAA03945.1;
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                                                                                                                                                                       Name=Short;
IsoId=P98155-2;
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D16529; B
D16530; B
D16531; B
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D16514; B
D16516; B
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D16508;
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PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS01089; LDLRA_2; 8.

BR PROSITE; PS050068; LDLRA_2; 18.

RM Glycoprotein; VLDL; Clolesterol metabolism; Lipid transport;

KW Eddocytosis; Coated pits; Transmembrane; Receptor; Signal;

KW Eddocytosis; Coated pits; Transmembrane; Receptor; Signal;

KW Eddocytosis; Coated pits; Transmembrane; Receptor; Signal;

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CYTOPLASMIC (POTENTIAL).

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 6.

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LDL-RECEPTOR CLASS A 7.

LDL-RECEPTOR CLASS B 1.

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REF-LIKE 3.

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REF-LIKE 3.

LDL-RECEPTOR CLASS B 5.

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Pred. No. 0.96;
7; Mismatches 38; Indels 1:
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nilarity 31.7%;
Conservative 7
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Neuron 24:481-489 (1999).
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MEDLINE=20036019; PubMed=10571241;
Hiesberger T., Trommsdorff M., Howell B.W., Goffinet A.M., Mumby M.C.,
Cooper J.A., Herz J., Reelin to VLDL receptor and ApoE receptor 2 induces
tyrosine phosphorylation of disabled-1 and modulates tau
phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Skeletal muscle;
MEDLINE-94283285; PubMed-8013374;
Gafvela M.E., Paavola L.G., Boyd C.O., Nolan P.M., Wittmaack F.,
Chawla A., Lazar M.A., Bucan M., Angelin B.O., Strauss J.F.;
"Cloning of a complementary deoxyribonucleic acid encoding the murine homolog of the very low density lipoprotein/apolipoprotein-E receptor: expression pattern and assignment of the gene to mouse chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 204-262 FROM N.A.
MEDLINE=95003355; PubMed=7919660;
Naggert J.K., Mu J.L.;
"The mouse very low density lipoprotein receptor (Vldlr) gene maps to chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation.
-!- SUBUNIT: Binds to the extracellular matrix protein Reelin.
-!- SUBUNIT: Binds to the extracellular matrix protein.
-!- TISSUE SPECIFICITY: ABBUDDANT IN HEART AND MUSCLE; LESS IN KIDNEY,
-!- TISSUE SPECIFICITY: LUNG, ADIPOSE TISSUE.
-!- SIMILARITY: Contains 8 LDL-receptor class A domains.
-!- SIMILARITY: Contains 3 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                      Li W.H., Chan L.;
"Mouse very-low-density-lipoprotein receptor (VLDLR) cDNA cloning,
tissue-specific expression and evolutionary relationship with the
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                    LDVR_MOUSE . STANDARD; PRT; 873 AA.
P98156, 064022.
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor (VLDL receptor)
VLDLR.
                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Heart;
MEDLINE=55101090; PubMed=7925422;
Oka K., Ishimura-Oka K., Chu M.J., Sullivan M., Krushkal J.,
Li W.H., Chan L.;
288 GSCIHGSRQCNGIRDC-VDGSD 308
                                                                                                                                                                                                                                                                                                                                                                                  low-density-lipoprotein receptor."
Eur. J. Biochem. 224:975-982(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm. Genome 5:453-455(1994)
                                                                                                                                                                                              Mus musculus (Mouse)
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LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 8.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 3.
LDL-RECEPTOR CLASS B 3.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 5.
LDL-RECEPTOR CLASS B 5.
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PROSITE; PS00010 ASX HYDROXYL; 2.
PROSITE; PS001186; EGF 2; 3.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01209; LDLRA 1; 8.
PROSITE; PS0068; LDLRA 2; 8.
Glycoprotein; VLDL; Cholesterol metabolism; Lipid transport; Endocytosis; Coaced pite; Transmembrane; Receptor; Signal; EGF-like domain; Repeat.
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LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
                                                                                                                                                                        InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000181; EGF_Ca.
InterPro; IPR000172; LDL receptor A.
InterPro; IPR000033; Ldl_receptor_rep.
Ffam; PF00008; EGF; 2.
Ffam; PF00008; Ldl_recept_b; B.
Ffam; PF00008; Jdl_recept_b; S.
Ffam; PR00051; Ldl_recept_b; S.
Ffam; PR00051; Ldl_recept_b; S.
RNNT; SM001192; LDLABCEPTOR.
SWART; SM001192; LDLABCEPTOR.
SWART; SM001192; LDLABCEPTOR.
EMBL, L33417; AAC37668.1; --
EMBL, U06670; AAA59384.1; --
EMBL, S73722; AAB32228.2; --
EMSL, I48952, I48952.
HSSP, P01130; IAJJ.
MGD, MGI:98935; Vldlr.
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EWBL outstation-the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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A Takhasahi S., Kawarabayasi Y., Nakai T., Sakai J., Yamamoto T.;
A Takhasahi S., Kawarabayasi Y., Nakai T., Sakai J., Yamamoto T.;
A Takhasahi S., Kawarabayasi Y., Nakai T., Sakai J., Yamamoto T.;
Tabbit very low density lipoprotein receptor: a low density
lipoprotein receptor-like protein with distinct ligand specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:9252-9256(1992).
C -- FUNCTION: Binds VLDL and transports it into cells by endocytosis.
C -- FUNCTION: Binds VLDL and transports it into cells by endocytosis.
C -- SUBGINIT: Binds to the extracellular matrix protein Reelin (By similarity).
C -- SUBGILLULAR LOCATION: Type I membrane protein.
C -- IISSUE SPECIFICITY: ABUNDANT IN HEART, MUSCLE, AND ADIPOSE
TISSUE.
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31.7%; Pred. No. 0.96;
ive 7; Mismatches 38; Indels 11; Gaps
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor (VLDL receptor).
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P -> L (IN REF. 3)
C -> S (IN REF. 2)
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228 QCGRQPVIHTKCPASEIQCGSGECIHKKWRCDGDPDCKDGSDEVNCPSRTCRPDQFECED 287
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N-LINKED (GLCNAC. ..) (POTENTIAL).
MM; CDF65441241A4B33 CRC64;
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Search completed: December 8, 2003, 09:14:12 Job time: 24.0606 secs

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Q9gpc4 drosophila Q8mp01 halocynthia Q9nc91 strongyloce P97883 rattus norv

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Stanssens P., Bergum P.W., Gansemans Y., Jaspers L., Laroche Y., Huang S., Maki S., Messens J., Lauwereys M., Cappello M., Hotez P.J., Lasters I., Vlasuk G.P.;

"Anticoagulant repertoire of the hookworm Ancylostoma caninum.";

Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).

EMBL, U30793; AAC47080.1; -.

InterPro; IPRO06209; EGF like.

InterPro; IPRO02219; TLL_Cysrich.

PROSITE; PS01186; EGF_2; 1.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last sequence update)
Anti-coagulant protein C2 precursor (Fragment).
Ancylostoma caninum (Dog hookworm).
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID=29170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Surface expression and ligand-based selection of cDNAs fused to filamentous phage gene VI."; Biotechnology 13:378-382(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. WEDLINE=98298519; PubMed=9634780; Jespers L.S., Messens J.H., De Keyser A., Ecckhout D., Jespers L.S., Messemans Y.G., Lauwereys M.J., Vlasuk G.P., van den Brande I., Gansemans Y.G., Lauwereys M.J., Vlasuk G.P.,
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MEDLINE=96312555; PubMed=8700900;
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Q962v8 ancylostoma
Q9ubb ancylostoma
Q1633 ancylostoma
Q16335 ancylostoma
Q16947 ancylostoma
Q16940 ancylostoma
Q814b8 caenorhabdi
Q9ult6 caenorhabdi
Q9dqd5 microplitis
Q81655 anophales s
Q81655 anophales s
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OBtOwO pimpla hypo
O16620 caenorhabdi
O45764 caenorhabdi
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                Compugen Ltd.
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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Q962Y8
Q9U9B1
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                                                                                                                                                                                                                                                                     1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                   8 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 67
                                                                                                                                                                              Gaps
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Harrison L.M., Cappello M.;
"Cloning of the major factor Xa inhibitor (AceAP-1) from Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryora; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma. NCGI_TaxID=53326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. "Arrison L.M., Cappello M.; "The molecular cloning of an ascaris type serine protease inhibitor
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Ancylostomatoidea, Ancylostomatidae, Ancylostomatinae, Ancylostoma.
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                                                                                  100.0%; Score 486; DB 5; Length 91; 100.0%; Pred. No. 1.2e-49;
                                                                                                                                                                              0; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF399710; AAK81733.1; -.
InterPro; IPR006209; EGF like.
InterPro; IPR002919; TIL_Cysrich.
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315722980EF723E7 CRC64;
10358 MW; ECB11CB4597C24DA CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Ancylostoma ceylanicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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20 102 AD
102 AA; 11834 MW;
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                                                                                                                                                                              84; Conservative
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                                                                                                                            Local Similarity
91 AA;
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SEQUENCE
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ID 0962V8
DT 01-D
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Ancylostomatoidea, Ancylostomatidae, Ancylostomatinae, Ancylostoma.
                                                                                                                                                                                                                                    Length 76;
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                                                                                                                                                                                                                                                                          Indels
from adult Ancylostoma ceylanicum hookworms.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF172653; AAD51336.1; -.
HSSP; P56682; ICCV.
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ANTICOAGULANT PROTEIN 6.
2DF0FDDBE7444F69 CRC64;
                                                                                                                                                                                 1 1
76 AA; 8385 MW; D35FCEF7C2088A53 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Anticoaqulant protein 6 precursor.
Ancylostoma caninum (Dog hookworm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 28.7%; Score 139.5; DB 5; Local Similarity 38.8%; Pred. No. 6.7e-09; nes 31; Conservative 12; Mismatches 16;
                                                                                                                                                                                                                                    Query Match 32.6%; Score 158.5; DB 5; Best Local Similarity 42.7%; Pred. No. 3.1e-11; Matches 35; Conservative 14; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                            58 RNKDDKCVSAEDCEL-DNMDFI 78
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RDRAGDCVTDEDCAIWDDMEFI 71
                                                                               InterPro, IPR006209; EGF like.
InterPro; IPR002919; TIL_Cysrich.
Pfam; PF01826; TIL; 1.
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EDGFYRDTVIGDCVKEEECD 91
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24 98 1
98 AA; 11048 MW;
                                                                                                                                       PROSITE; PS01186; EGF 2; 1.
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SEQUENCE
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                                                                                 Query Match
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                           MEDLINE=93274118; PubMed=8501344;
Cappello M., Clyne L.P., McPhedran P., Hotez P.J.;
"Ancylostoma factor Xa inhibitor: partial purification and its
identification as a major hookworm-derived anticoagulant in vitro.";
J. Infect. Dis. 167:1474-1477(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ancylostoma caninum (Dog hookworm)..
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostoma.
                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97039675; PubMed=8885227;
Cappello M., Hawdon J.M., Jones B.F., Kennedy W.P., Hotez P.J.;
Cappello M., Hawdon J.M., Jones B.F., Kennedy W.P., Hotez P.J.;
Ancylostoma caninum anticoaquiant peptide: cloning by PCR and
expression of soluble, active protein in E. coli.";
Mol. Biochem. Parasitol. 80:113-117(1996).
EMBL, U18305; AAC47318.1; -.
InterPro; IPR006209; EGP_like.
InterPro; IPR006209; TIL_Cysrich.
PEam; PF01826; TIL; 1.
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Proc. Natl. Acad. Sci. U.S.A. 92:6152-6156(1995).
EMBL, U46550; AAA87584.1; -.
InterPro: IPR006509; EGF like.
InterPro: IPR002919; TIL_Cysrich.
Pfam; PP01826; TIL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 28.3%; Score 137.5; DB 5; Length Similarity 42.5%; Pred. No. 9.2e-09; 31; Conservative 11; Mismatches 26; Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biochem. Parasitol. 0:0-0(1996).
                                                                                                  Ancylostoma caninum (Dog hookworm).
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MEDLINE=95320231; Pubmed=7597095;
                                                                         Anticoagulant peptide (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticoagulant peptide isoform 2.
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58 TVIGDCVREEECD 70
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                                                                                                                                                                       NCBI_TaxID=29170;
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Lasters I., Vlasuk G.P.,
"Anticoagulant repertoire of the hookworm Ancylostoma caninum.";
Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).
EMBL; U30795; AA47082.1; -.
InterPro; IPR002919; EIL_Cysrich.
Pfam; PF01826; TIL,
PROSITE; PS01186; EGF_2; 1.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
Anti-coagulant protein 5 precursor.
Ancylostoma caninum (Dog hookworm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostoma.
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23 100 ANTICOAGULANT PROTEIN 5.
100 AA; 11359 MW; DE9CB76729719A42 CRC64;
PROSITE; PS01186; EGF_2; 1.
SEQUENCE 91 AA; 10324 MW; E627F11E89B3EB4A CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Y69H2.3d.
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                                                                                                                      1.1e-08
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                                                                                      ch 28.3%; Score 137.5;
1 Similarity 42.5%; Pred. No. 1.1e
31; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                     60 K-DDKCVSAEDCE 71
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72 TVIGDCVREEECD 84
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81 TVIGDCVREEECD 93
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SEQUENCE FROM N.A.
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65 VSAEDC 70
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                                                                 SEQUENCE FROM N.A.
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Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                  Query Match 25.7%; Score 125; DB 5; Length 432; Best Local Similarity 36.1%; Pred. No. 1.5e-06; Matches 26; Conservative 10; Mismatches 16; Indels ;
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                                                               "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
SMBL; 289877; CAD55617.1; -.
Hypothetical protein.
SRQUENCE 432 AA; 46710 MW; F4C99F0221709D67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
        McMurray A.A.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; 29877; CAB54472.2; -.
Hypothetical protein.
SEQUENCE 537 AA; 58089 MW; 96F837138278D168 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created
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                                              MEDLINE=99069613; PubMed=9851916;
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414 NSGKCVTQNDCD 425
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SEQUENCE FROM N.A.
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Q9U1T6;
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                                                         none;
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Q9DQD5
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative salivary secreted serine procease inhibitor.
Anopheles stephensi (Indo-Pakistan malaria mosquito).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=30069;
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Trudeau D., Witherell R.A., Strand M.R.;
Trudeau D., Witherell R.A., Strand M.R.;
Trudeau D., Witherell R.A., Strand M.R.;
Trudeactization of two novel Microplitis demolitor polydnavirus
mRNAs expressed in Pedudoplusia includens haemocytes.";
J. Gen. Virol. 81:3049-3058(2000).
InterPro; IPR06209; AG24547.11.
InterPro; IPR002919; TIL_Cysrich.
PROSTIE; PS01186; TIL, 1.
PROSTIE; PS01186; EGF 1:1.
SEQUENCE 102 AA; 11572 MW; F7FBB7CEAF77E9F9 CRC64;
                                                        Microplitis demolitor polydnavirus.
Viruses; dsDNA viruses, no RNA stage; Polydnaviridae; Bracovirus.
NCBI_TaxID=53988;
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TISSUE-Salivary gland;
Valenzuela J.G., Francischetti I.M.B., Pham V.M., Garfield M.K.,
Ribeiro J.M.C.;
Ribeiro J.M.C.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AX162234; AAO06826.1; -.
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11572 MW; F7FBE7CEAF77E9F9 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pi201.
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79 TCIKVEDCPNVSENLEF 95
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Matches 26; Conservative
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01-JUN-2002 (TrEMBLrel, 21, 01-JUN-2002 (TrEMBLrel, 21, 01-OCT-2002 (TrEMBLrel, 22,
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                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    Pimpla hypochondriaca.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=135724;
                            66 SAEDC 70
                                                                74 -TKDC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                          SCTT WELL SOLD DESCRIPTION OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEKYDSCGSKECDK-----KCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYR 58
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                                                                                                                                                                                                                                                                               "Identification of interactions between trefoil peptides and members of the mucin protein family using the yeast two-hybrid system."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ010752; CAA09343.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNKDDKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Boag P.R., Ranganathan S., Newton S.E., Gasser R.B.;

"Identification of a male-specific nematode protein with two trypsin like inhibitor domains." Is bubmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF399936; AAN32637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 POTENTIAL.
154 PUTATIVE TRYPSIN-LIKE INHIBITOR PROTEIN
16564 MW; A7F566E3957DA819 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromadorea; Rhabditida; Strongylida;
                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                             TISSUE-Stomach;
Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.8%; Score 120.5; DB 11; Length 499; 30.1%; Pred. No. 5.7e-06; ive 8; Mismatches 35; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54190 MW; 04F89EF4F23EE61E CRC64;
                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update
Putative trypsin-like inhibitor protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4e-06;
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Strongyloidea, Chabertiidae, Oesophagostomum.
NCBI_TaxID=61180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%; Score 119.5; I 36.9%; Pred. No. 2.4e-
tive 8; Mismatches
                                                          Gastric mucin-like protein (Fragment)
GASTRIC MUCIN-LIKE.
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    Created)
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InterPro; IPR001846; VWF_D.
01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2002 (TrEMBLrel. 22,
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Pfam; PF00094; vwd; 1.
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les 25; Conserv
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                                                                                                                                                                 NCBI_TaxID=10090;
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Matches
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24 CGPNRVYKSCGT-GCPETC-----ENPDPDC-DRACHQGCFCSKGLLQDIDGNCI
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Venom secretory;

Barkinson N.M., Richards E.H., Conyers C., Smith I., Edwards J.P.,

"Analysis of venom constituents from the parasitoid wasp Pimpla
hypochondriaca and cloning of a cDNA encoding a venom protein.";

Insect Blochem. Mol. Biol. 0:0-0(0).

Biol. 50-000 Fig. 10-0000 Fig. 10-00000 Fig. 10-0000 Fig. 10-00000 Fig. 10-0000 Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
Ichneumonidae; Pimplinae; Pimpla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.1%; Score 117; DB 5; Length 77; 35.4%; Pred. No. 2.3e-06; ive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE-RICH VENOM PROTEIN 6889CB5F40D63DD6 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical protein F36H9.4.
                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
77 AA.
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STRAIN=Bristol N2;
Wilson R., Dante M., Kramer J., Twyman B.;
                                                                                                                                                                                                                                                                                                                                            Cysteine-rich venom protein 6 precursor.
                                                                                                                                             Created)
       PRT;
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MEDLINE-99069613; PubMed-9851916;
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Search completed: December 8, 2003, 09:18:37 Job time : 90.2424 sec8

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Run on:

Sequence:

Searched:

Database

Result No.

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TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09498272;
Publication No. US20030113890A1
GENERAL INFORMATION;
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
MOyle, Matthew
US-09-498-272-27
US-09-498-272-44
US-09-498-272-44
US-09-498-272-41
US-09-498-272-23
US-09-498-272-21
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILLING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILLING DATE: October 17, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              storage
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STATE: California
COUNTRY: U.S.A.
    US-09-498-272-59
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    (without alignments)
209.232 Million cell updates/sec
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                                                                                                                                              8, 2003, 09:18:46; Search time 74.6667 Seconds
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Sequence 46,
Sequence 48,
Sequence 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45,
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Sequence 5
Sequence 6
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Sequence
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                                                                                                                                                                                                                                  US-09-498-556C-59
486
1. KATMQCGENEKYDSCGSKEC......VSAEDCELDNMDFIYPGTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Ggn2_6'ptodata/2'/pubpaa/US07_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/PCT' NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US06_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US06_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US07_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/PCTUB' PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US08_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US08_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US08_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US08_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US09_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US09_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US108_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US108_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US108_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US108_PUBCOMB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US10_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US10_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US10_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US10_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US10_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US60_NEW PUB.pep:*
'Ggn2_6'ptodata/2'/pubpaa/US60_NEW PUB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-498-272-128
US-09-498-272-25
US-09-498-272-49
US-09-498-272-46
US-09-498-272-46
US-09-498-272-48
US-09-498-272-24
US-09-498-272-24
US-09-498-272-53
US-09-498-272-63
US-09-498-272-63
US-09-498-272-63
US-09-498-272-64
US-09-498-272-64
US-09-498-272-64
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                                                                                                                                                                                                                                                                                                                                                                                          684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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41.6
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486
212
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212
202
201
201
197.5
193.5
193.5
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Perfect score:
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8 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 91;
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TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 486; DB 11; Best Local Similarity 100.0%; Pred. No. 9.4e-42; Matches 84; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                         TANAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REPERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEFA: (213) 955-0440
TELEFA: (7-3510
TELEFA: (7-3510
TELEFA: (7-3510
TELEFA: (7-3510
TELEFA: (7-3510
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Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) SEQUENCE DESCRIPTION: SEQ ID NO: 128: US-09-498-272-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 25, Application US/09498272; Publication No. US20030113890A1; GENERAL INFORMATION: APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDKCVSAEDCELDNMDFIYPGTRN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DDKCVSAEDCELDNMDFIYPGTRN 84
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-498-272-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muyic, Meter W.
Bergum, Peter W.
BITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEFHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (723) 955-0440
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Storage COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
                   FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 59 US-09-498-272-59
  APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSE: Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 128, Application US/09498272; Publication No. US20030113890A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-498-272-128
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Gaps ; 0

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6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD---CVCEEGFYRNKDD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.6%; Score 212; DB 11; 50.0%; Pred. No. 3e-14;
                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
PPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRY APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ); ORGANISM: Ancyclostoma ceylanicum; SEQUENCE DESCRIPTION: SEQ ID NO: 49: US-09-498-272-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: June 5, 1995
APPLICATION WUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 62, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lauwereys, Marc Josef
Laroche, Yves Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 82 amino acids
                                                                                                                                                                                                                                                              storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49
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  NUMBER OF SEQUENCES: 35
                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
                        CORRESPONDENCE ADDRESS
                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SCVESDDCEYDNMDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches '38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-498-272-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CGSNERYSDCGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCEDGFYRNKKG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.6%; Score 212; DB 11; Length 82;
50.0%; Pred. No. 3e-14;
tive 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Massens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yamnick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                   ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                         COMPUTER: IBM Compatible
ODERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04.Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Ancyclostoma ceylanicum SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: October 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: (213) 489-16(
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 82 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ::||| |||||||
59 SCVESDDCEYDNMDFI 74
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergum,
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Bergum, Peter W.
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                         Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                     Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 86 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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43.6%; Score 212; DB 11; Length 171;
Best Local Similarity 50.0%; Pred. No. 6.4e-14;
Matches 38; Conservative 11; Mismatches 19; Indels
                                                                                                   Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
Gansemans, Yannick Georges Jozef Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000

PRIOR APPLICATION NUMBER: US/05/13231
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Ancyclostoma ceylanicum
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-498-272-46
; Sequence 46, Application US/09498272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 171 amino acids
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INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
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148 SCVESDDCEYDNMDFI 163
                                                                                                                                                                                                                                                                                                                                                                  CITY: LOB Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                             4; Gaps
                                                                                                      Length 86;
                                                                                                                                                       Indels
                                                                                                Query Match
41.6%; Score 202; DB 11;
Best Local Similarity 47.4%; Pred. No. 3.2e-13;
Matches 37; Conservative 15; Mismatches 22;
ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 46.
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Conservative
  38;
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    Matches
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                                                                                                                                                                                                                                                                                                                                                         Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                     INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.4%; Score 201; DB 11; 48.1%; Pred. No. 4.2e-13;
                                                                                                                                                                                                                                              Lauwereys, Marc Josef
Laroche, Yves Rene
Laspers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                   Sequence 48, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/498,272 FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 Messens, Joris Hilda Liever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 216/270 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Ancyclostoma ceylanic; ; SEQUENCE DESCRIPTION: SEQ ID NO: 48 US-09-498-272-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
Site 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 89 amino acids
: | | : | : | : | | 65 KGECVTDDVCQEDFMEFI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
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3 TMQCGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRN 59
                                                                            7 THACGLNEYFAECGNMKECEHRCN-EEENEERDEERITACLIRVCFRPGACVCKDGFYRN
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 6, 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERfect 5.1
CURRENT APPLICATION DATA:
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/498,272 FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lauwereys, Marc Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                  Stanssens, Patrick Er
Messens, Joris Hilda
                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 108 amino acids
                                                                                                                                                                                         66 RTGSCVEEDDCEYENMEFI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bergum, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            60 KDDKCVSAEDCELDNMDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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4; Gaps

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5 QCGENEKYDSCGSKECDKKCKYDGVEEEDD--EEPNVPCLVRVCHQ--DCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                          S KCGPGERLDCANKKPCEPKCKIETSEEBDDDVEDTDVRCLVRVCERPLKCICKDGYYRNK
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TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            Query Match 40.9%; Score 199; DB 11; 3
Best Local Similarity 46.2%; Pred. No. 6.4e-13;
Matches 36; Conservative 16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
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PRICATION NUMBER: US/09/498,272
PRICATION NUMBER: PCT/US95/13231
PRILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER EXAMBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                                                                                                                                                                                                ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
                                                                            LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DDKCVSAEDCELDNMDFI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||: |: ||: || |: || 65 KGECVTDDVCQEDFMEFI 82
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS
                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   US-09-498-272-45
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US-09-498-272-43
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                                                                                                                                                                                                                                                      26 TNACGLNEYFAECGNMKECEHRCN-EEENEERDEERITACLIRVCFRPGACVCKDGFYRN 84
                                                                                                                                                                                                                            3 TMQCGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRN
                                                                                                                                                                              4
                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INTLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                           24; Indels
                                                                                                                           41.4%; Score 201; DB 11;
48.1%; Pred. No. 5.1e-13;
tive 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gansemans, Yannick Georges Jozef
Moyle, Matthew
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APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Fb-2000

PRIOR APPLICATION NUMBER: US/05/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INCORMATION:
ATTORNEY/AGENT INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
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; ORIGINAL SOURCE:
    ORGANISM: Ancyclostoma ceylanicum
    SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-498-272-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSE: Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/09498272
Publication No. US2003113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                     : || :||| :||| :|| :|| :|| :|| RTGSCVEEDDCEYENMEFI 103
                                                                                                                                                                                                                                                                                                                        60 KDDKCVSAEDCELDNMDFI 78
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                   Query Match
Best Local Similarity 48.1%
Matches 38; Conservative
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APPLICATION NUMBER: US/09/498,272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ECGPHERLD-CGNKKPCERKCKIETSEEDDYEEGTERFRCLLRVCDQPYECICDDGYYR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.6%; Score 197.5; DB 11; Best Local Similarity 46.2%; Pred. No. 9.3e-13; Matches 37; Conservative 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lauwereys, Marc Josef
Laroche, Yves Rene
Laspers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,188
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0410
TELEX: SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
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FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKDDKCVSAEDCELDNMDFI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 NKKGECVIDDVCQEDFMEFI 84
                                                                                                                                                                                                                          LENGIH: 88 amino acids
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
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1 KATMQCGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVC-HQDCVCEEGFYR 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.2%; Score 195.5; DB 11; Length 84; 50.0%; Pred. No. 1.4e-12; ive 11; Mismatches 26; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergum, Peter W. TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INHIBITORS AND ANTICOAGULANT
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Laroche, Yves Rene
Laspers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
APPLICATION NUMBER: 08465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/09498272
Publication No. US20030113890A1
                                                                                                                                                                                                                                                                            TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 NKDDKCVSAEDCELDNMDFI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NKKGQCVTRDDCEYDNMEII 79
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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NKKGQCVTRDDCEYDNMEII 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-498-272-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KSAKKCGLNEKLD-CGNLKACEKKCSDLDNEEDYKEEDESKCRSRECSRRVCVCDEGFYR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/09498272; Sequence 51, Application No. US20030113890A1; Publication No. US20030113890A1; ENDICANT: VISENE, George Phillip Stanssens, Parrick Eric Hugo Messens, Joris Hilda Lieven Lauvereys, Marc Josef Lauvereys, Marc Josef Lauvereys, Laurent Stephane Jespers, Laurent Stephane Gansemans, Yannick Georges Jozef Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.2%; Score 195.5; DB 1
50.0%; Pred. No. 2.8e-12;
tive 11; Mismatches 26
              PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486, 399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466, 397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461, 965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461, 965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
TELEBRAK: (213) 489-1600
TELEFRAK: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NKDDKCVSAEDCELDNMDFI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :||::||| |||: |
NKKGQCVTRDDCEYDNMEII 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-498-272-51
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1 KATMOCGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVC-HQDCVCEEGFYR 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Publication No. US20030113890A1

GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip

Stanssens, Patrick Eric Hugo
Messens, Joria Hilda Lieven
Lauwereys, Marc Josef

Laroche, Yves Rene
Jespersh, Laurent Stephane
Gansemans, Yamick Georges Jozef

Moyle, Matthew.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.8%; Score 193.5; DB 1
50.0%; Pred. No. 2.2e-12;
                                                                                                                                                               PAPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 11; Mismatches
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, VUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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1 KATMQCGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVC-HQDCVCEEGFYR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bergum, Peter W.
TITLE OF INVENTION: NEWATODS-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.3%; Score 186; DB 11;
50.0%; Pred. No. 1.3e-11;
tive 11; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/13231
PILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                           UTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 216/270 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8, 2003, 09:34:03
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SEQUENCE DESCRIPTION: SEQ ID NO: 52
                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 NKDDKCVSAEDCELDNMDFI 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              storage
                                                                                                   NUMBER OF SEQUENCES: 356
                                                                                                                                                                                           Suite 4700
                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0*
Matches 40; Conservative
                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December Job time: 75.6667 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 39.8%; Score 193.5; DB 11; Best Local Similarity 50.0%; Pred. No. 4.4e-12; Matches 40; Conservative 11; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yamick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                               PRIORAGE TO THE CATAINAN UNIVERSE TO A PRELICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/41,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                                                                                                                                                                MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
  STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 NKKGQCVTRDDCEYDNMEII 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NKDDKCVSAEDCELDNMDFI
                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-498-272-64
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Gaps

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(OTYZU) NNAJB 32A9 21HT

Nematode extracted Mature nematode ex A. caninum nematod

Ancylos

AcaNAP44.

Nematode extracted Mature nematode ex Nematode extracted

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AceNAP4. Ancylost

A. ceylanicum ne Mature nematode

A. ceylanicum nema Mature nematode ex A. caninum nematod

AcaNAP25. Ancylos Nematode extracted Mature nematode ex A. caninum nematod Ancylos

AcaNAP45.

Nematode extracted Mature nematode ex Mature nematode ex A. caninum nematod AcaNAP47. Ancylos Nematode extracted Mature nematode ex Nematode extracted

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

08 08

Minimum Maximum

Database

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AcaNAP23. Ancylos
Nematode extracted
Mature nematode ex
Mature nematode ex
A. caninum nematod
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Mature nematode ex
AduNAP7. Ancylost
Nematode extracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/FF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mature nematode extracted anticoagulant protein AcaNAPc2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gansemans YGJ, Jespers LS, Laroche YR;
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                                                                           AAY30419
AAB15304
AAR91708
AAY30408
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AAY30436
AAB15321
                                                                                                                                                                        AAY30398
AAB15292
                                                                                                                                                                                                                                                     AAR91707
AAY30406
                                                                                                                                                                                                                                                                                            AAY30416
AAB15301
                                                                                                                                                                                                                                                                                                                                  AAR91705
AAY30404
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR91711
AAY30409
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AAY30417
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940S-0461965.
950S-0465380.
950S-0486397.
950S-0486399.
95WO-US13231.
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18-OCT-1994;
05-JUN-1995;
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05-JUN-1995;
05-JUN-1995;
17-OCT-1995;
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AAY30432;
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  AcanAPc2. Arcylos
Nemacode extracted
Nemacode extracted
A. caninum nematod
Nemacode extracted
Mature nematode ex
A. ceylanicum nema
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                                                                                                                           8, 2003, 09:13:30 ; Search time 114.545 Seconds (without alignments) 116.399 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                                                                                                                                                                                                                                               KATMQCGENEKYDSCGSKEC.....VSAEDCELDNMDFIYPGTRN
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAB15317
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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486
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(CORV-) CORVAS INT INC
(CORV-) CORVAS INT INC
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                                                                   N-PSDB; AAA73373
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05-JUN-1995;
05-JUN-1995;
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17-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AcaNAPc2.
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                       protein (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/Fr. The specification for factor VIIa/Fr. The specification for factor VIIa/Fr selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the activated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating proportion of clotting effected by the isolated protein in each of the rand aptr assay, with respect to a baseline clotting value for cach assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a calculating a protein give method is calculating at the aptr prolongation ratio, where a ratio at least one is indicative of factor VIIa/FF inhibitory activity. The method is useful for determining if a protein has factor VIIa/FF inhibitory
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. caninum nematode-extracted anticoagulant protein AcaNAPc2 (mature).
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematode-extracted anticoagulant protein; AcaNAPc2; blood clotting; canine hookworm; thrombosis; vaccine.
                                                                                                                 sequence represents a nematode extracted anticoagulant
                                                         an isolated protein for Nematode-extracted Anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 486; DB 20; Length 84; 100.0%; Pred. No. 1.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
  Stanssens PEH;
                                                                                          Disclosure; Columns 142-144; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
  Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB15317 standard; Protein; 84 AA
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940S-0326110.
950S-0461965.
950S-0465380.
950S-0486397.
  Lauwereys MJ, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0249451
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                                                                                                                                                                                                                                                                                                                                                                                 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ancyclostoma caninum
                                 WPI; 1999-539569/45
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                     84 AA;
                                                         Screening an iso
Protein domains
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17-APR-1997;
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             Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the Ancyclostoma caninum nematode-extracted anticoagulant protein AcaNAPc2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated incravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                      PEH, Jespers LS, Gansemans YGJ, Moyle M;
LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                     New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 486; DB 21; Length 84; 100.0%; Pred. No. 1.7e-38; ive 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91701 standard; Protein; 91 AA
                                                                                                                                                                                                                                                                                                                                    Example A; Fig 16; 197pp; English.
                            Stanssens PEH,
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95US-0461965.
95US-0465380.
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(first entry)
Lauwereys MJ, Stand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancylostoma caninum
                                                                                                                     WPI; 2000-531359/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nematode parasites
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1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 KATMÓCGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                       Lauwereys MJ, Laroche YR;
                                                                                                                                                                                                                                                                                                                                                                                             They can also be used as immunogens in prophylactic and therapeutic vorm. Vaccines against parasitic worm infection. The proteins may double the clotting time of human plasma in prothrombin time assays when present at 10-50 nMol, and double the clotting time of human plasma in prothrombin time assays plasma in activated partial thrombin time assays at 10-100 nMol.
                                                                                                                                                                                                                                                           activity, isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or in vivo diagnostic agents. The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The anticoagulant proteins are pref. derived from Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligomosmoides polygyrus.

The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv., do not specifically inhibit the activation of factor VIIa in the absence of TF and do not specifically inhibit prothrombinase. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                            Proteins with anticoagulant and/or serine protease inhibitory activity - isolated from nematodes and useful to inhibit blood
                                                                                                                                                                                                                                           Proteins with anticoagulant and/or serine protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematode extracted anticoagulant protein AcaNAPc2.
                                      Bergum PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 486; DB 17;
100.0%; Pred. No. 1.9e-38;
ive 0; Mismatches 0;
                     Messens JHL,
Moyle M, Be
                                                                                                                                                                                                    Claim 89 + 96; Fig 9; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDKCVSAEDCELDNMDFIYPGTRN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30393 standard; Protein; 91 AA
                 Stanssens PEH,
Gansemans YGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 84; Conservative
                                                                        WPI; 1996-222007/22.
N-PSDB; AAT12947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA;
               Vlasuk GP,
Jespers LS,
                                                                                                                                                activity -
coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USS955294-A.
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셤
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protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF. The specification of containing the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin [PT] assay and an ex vivo activated partial thromboplastin time (APTT) assay, calculating a prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, where prolongation of clotting is calculated as fold clevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where calculating a PT to aPTT prolongation ratio, where a ratio, and calculating a PT to aPTT prolongation ratio, where a ratio, at least one is indicative of factor VIIa/FF inhibitory activity. The method is useful for determining if a protein has factor VIIa/FF inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                       Screening an isolated protein for Nematode-extracted Anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a nematode extracted anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 486; DB 20; Length 91; 100.0%; Pred. No. 1.9e-38; ive 0; Mismatches 0; Indels
                                                                                                                                                                                      , Laroche YR;
Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematode extracted anticoagulant protein AcaNAPc2.
                                                                                                                                                                                  Jespers LS,
Moyle M, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                          Example 13; Fig 9; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDKCVSAEDCELDNMDFIYPGTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDKCVSAEDCELDNMDFIYPGTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY30454 standard; Protein; 91 AA
                              94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
                                                                                                                                                                                Bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
                                                                                                                  95WO-US13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
                                                                                                                                                  (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                     WPI; 1999-539569/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAZ99999.
                                                                                                                                                                                                                                                                                                                         Protein domains
                              18-OCT-1994;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                 17-0CT-1995
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                                                                                                                                                                                                                       Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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Gaps

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67

96US-0634641.

19-APR-1996;

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Ancyclostoma caninum.
                       US6087487-A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY30399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                        The present sequence represents a nematode extracted anticoagulant protein (NAP). The protein has activity as an anticoagulant and/or serine protein in the protein contains at least one NAP domain which has selective inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIA/TF specification describes a method for screening an isolated protein at least one domain for factor VIIA/TF selective inhibitory activity. The method comprises determining the time to clotting an isolated protein at least one domain captured partial thromboplastin time (APT) assay and an ex vivo activated partial thromboplastin time (APT) assay and an ex vivo prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay with respect to a baseline clotting value for each assay, where prolongation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and a doubling of clotting time is deemed a two-fold elevation; and a calculating as PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIA/TF inhibitory activity. The method is useful.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 KATMQCGENEKYDSCGSKECDKKCKYDGVEZEDDEEDNVPCLVRVCHQDCVCEGGFYRNK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematode-extracted anticoagulant protein; AcaNAPc2; blood clotting; canine hookworm; thrombosis; vaccine.
                                                                                                                                                                                                                                                   Screening an isolated protein for Nematode-extracted Anticoagulant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. caninum nematode-extracted anticoagulant protein AcaNAPc2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 91;
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                                                                                                                                                                               Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 486; DB 20; 100.0%; Pred. No. 1.9e-38;
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                                                                                                                                                                                                                                                                                      Disclosure; Columns 175-176; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDKCVSAEDCELDNMDFIYPGTRN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB15346 standard; Protein; 91 AA
                                                          96US-0634641.
94US-0326110.
95US-0461965.
                                                                                              95US-0465380.
95US-0486397.
95US-0486399.
                                                                                                                                                                     bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                   96US-0634641
                                                                                                                                 95WO-US13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
                                                                                                                                                         (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                             WPI; 1999-539569/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AA;
                                                                                                                                                                                                                                                                 Protein domains
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                                     19-APR-1996;
                                                                                                                                 17-0CT-1995;
              21-SEP-1999
                                                            19-APR-1996
                                                                                                35-JUN-1995
                                                                                                          05-JUN-1995
                                                                                    35-JUN-1995
                                                                                                                      05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB15346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity
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AAB15346
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The present sequence is the Ancyclostoma caninum nematode-extracted anticoagulant protein AcaNAPc2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminanted intravascular coaqulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Gansemans YGJ, Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 486; DB 21;
ilarity 100.0%; Pred. No. 1.9e-38;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   PEH, Jespers LS, Ganse
LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDKCVSAEDCELDNMDFIYPGTRN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 11, 197pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30399 standard; Protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         Stanssens PEH,
                                                                                                           95WO-US13231.
97US-0809455.
94US-0326110.
95US-0465380.
95US-0465380.
95US-0486399.
                                                        99US-0249451
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergum PW, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ancylostoma ceylanicum.
                                                                                                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-531359/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nematode parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA73373
                                                                                                                                                                                                                                                                                                                                                                                                      Lauwereys MJ,
                                                     12-FEB-1999;
                                                                                                              17-OCT-1995;
                                                                                                                                                                         .8-OCT-1994;
                                                                                                                                                                                                                               05-JUN-1995
                                                                                                                                                                                                                                                                                        05-JUN-1995
11-JUL-2000
                                                                                                                                                                                                       35-JUN-1995
                                                                                                                                               17-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The present sequence represents a nematode extracted anticoagulant protein has activity as an anticoagulant and/or serine proteins (NAP). The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises certaining the time to clotting effected by a concentration of the confidence of isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (PT) assay and an ex vivo activated partial thromboplastin time (PT) assay, and ex vivo cativated partial thromboplastin time (PT) assay, and ex vivo prothrombin time (PT) assay and an ex vivo cativated partial thromboplastin time (PT) assay, and ex vivo cativated protein in each of the PT and assay, where prolongation of clotting is calculating value for each assay, where prolongation of clotting is calculated as fold clavation of clotting time relative to a baseline clotting value, where catoulating a PT to aPTT prolongation ratio, where a ratio at least calculating a PT to aPTT prolongation ratio, where a ratio at least cone is indicative of factor VIIa/FF inhibitory activity. The method is useful for determining if a protein has factor VIIa/FF inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CGSNERYSDCGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCEDGFYRNKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCBEGFYRNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.6%; Score 212; DB 20; Length 82; 50.0%; Pred. No. 9.1e-13; ive 11; Mismatches 19; Indels
     serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                             Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Columns 135-136; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB15293 standard; Protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                              pergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                                                                                                                                                                                                                95US-0465380.
95US-0486397
                                                                                                                                                                              96US-0634641
94US-0326110
                                                                                                                                             96US-0634641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 50.0
ses 38; Conservative
                                      Ancylostoma ceylanicum
                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-539569/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 AA;
                                                                                                                                             19-APR-1996;
                                                                                                                                                                                                                                                                     05-JUN-1995;
                                                                       US5955294-A.
                                                                                                          21-SEP-1999
                                                                                                                                                                                                                 35-JUN-1995;
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Matches
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AAB15293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/Fr. The specification for factor VIIa/Fr selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo protrombin time (FT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CGSNERYSDCGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCEDGFYRNKKG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CGENEKYDSCGS-KECDKKCKYDGVEBEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a nematode extracted anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematode extracted anticoagulant protein; NAP; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 43.6%; Score 212; DB 20; Length 82;
1 Similarity 50.0%; Pred. No. 9.1e-13;
38; Conservative 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature nematode extracted anticoagulant protein AceNAP4d2
                                                                                                                                                                                                                                                                                                    , Laroche YR;
Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 111-112; 197pp; English.
                                                                                                                                                                                                                                                                                                    Jespers LS,
                                                                                                                                                                                                                                                                                                                     Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY30422 standard; Protein; 82 AA.
                                                                                                                                    94US-0326110
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
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                                                                                                                                                                                                                                                                                                  Gansemans YGJ,
I, Messens JHL,
                                                                                      96US-0634641
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                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC.
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Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                   Lauwereys MJ,
Vlasuk GP,
                                                                                  19-APR-1996;
                US5955294-A.
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17-0CT-1995;
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05-JUN-1995
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05-JUN-1995
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canine hookworm; thrombosis; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the Ancyclostoma ceylanicum nematode-extracted anticoagulant protein AceNAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infaction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CGSNERYSDCGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCEDGFYRNKKG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                     PEH, Jespers LS, Gansemans YGJ, Moyle M;
LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. ceylanicum nematode-extracted anticoagulant protein AceNAP4d2 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematode-extracted anticoagulant protein; AceNAP4d2; blood clotting;
A. ceylanicum nematode-extracted anticoagulant protein AceNAP4d2 #1
                      Nematode-extracted anticoagulant protein; AceNAP4d2; blood clotting
                                                                                                                                                                                                                                                                                                              New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 43.6%; Score 212; DB 21; Length 82; l Similarity 50.0%; Pred. No. 9.1e-13; 38; Conservative 11; Mismatches 19; Indels
                                canine hookworm; thrombosis; vaccine
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 197pp; English
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                                                                                                                                                                                                                                                         Stanssens PEH,
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                                                                                                                                                    970S-0809455.
94US-0326110.
95US-0461965.
95US-0465380.
                                                                                                                       99US-0249451
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59 SCVESDDCEYDNMDFI
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                                                                                                                                                                                                                                                                    Messens JHL,
                                                       Ancyclostoma ceylanicum
                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                         WPI; 2000-531359/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 AA;
                                                                                                                                                                                                                                                         Lauwereys MJ,
                                                                                                                       12-FEB-1999;
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Best Local
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The present sequence is the Ancyclostoma ceylanicum nematode-extracted anticoagulant protein AceNAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atheroselerotic plaque, acute myocardial infarction, angina, thrombolyic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gansemans YGJ, Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature nematode extracted anticoagulant protein AceNAP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lauwereys MJ, Stanssens PEH, Jespers LS, Ganse
Bergum PW, Messens JHL, LaRoche YR, Vlasuk GP;
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ilarity 50.0%; Pred. No. 9.1e-13;
Conservative 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30435 standard; Protein; 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine against nematode parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 16; 197pp; English
                                                                                                                                                                                                                         95WO-US13231.
97US-0809455.
94US-0326110.
95US-0465380.
95US-0486397.
95US-0486399.
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                                                                                                                                                                         99US-0249451
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Ancyclostoma ceylanicum
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS
                                                                                                                                                                         12-FEB-1999;
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                                                      US6087487-A.
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6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins with anticoagulant and/or serine protease inhibitory activity, isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or in vivo diagnostic agents. The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. levels in biological fluids, eg. to detect mammalian infection with a parasitic worm. They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The anticogulant proteins are pref. derived from Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligomosmoides polygytus.

The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv., do not specifically inhibit the activation of factor VIIa in the absence of TF and do not specifically inhibit prothrombinase. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double the clotting time of human plasma in prothrombin time assay when present at 10-50 nMol, and double the clotting time of human plasma in activated partial thrombin time assays when present at 10-100 nMol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins with anticoagulant and/or serine protease inhibitory activity - isolated from nematodes and useful to inhibit blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.6%; Score 212; DB 17; Length 190; 50.0%; Pred. No. 2.1e-12; ive 11; Mismatches 19; Indels
AcaNAP; HpONAP; NamNAP; AceNAP; AduNAP; anticoagulant; nematode-extracted anticoagulant protein; serine protease; nematode; thrombosis; parasitic worm.
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Moyle M, Be
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                  109..190
/label= AceNAP4d2
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                                                                                                                                          1..108
/label= AceNAP4d1
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95US-0461965.
95US-0465380.
95US-0486397.
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Gansemans YGJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC.
                                                                               Ancylostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-222007/22.
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05-JUN-1995;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                 25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vlasuk GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                       Key
Domain
                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPT) assay; calculating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold a doubling of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation, and calculating a PT to aPTT prolongation ratio, where a ratio a telast one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a nematode extracted anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.6%; Score 212; DB 20; Length 171; 50.0%; Pred. No. 1.9e-12; ive 11; Mismatches 19; Indels 8
                                                                                                                                                                                                                                                                                                                                          , Laroche YR;
Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                          Jespers LS,
                                                                                                                                                                                                                                                                                                                                                             Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 17; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR91710 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 SCVESDDCEYDNMDFI 163
                                                                                                                                                   940S-0326110.
950S-0461965.
950S-0465380.
950S-0486397.
                                                                                                                                                                                                                                                                                                                                        Gansemans YGJ,
I, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 KCVSAEDCELDNMDFI 78
                                                                                              96US-0634641
                                                                                                                                    96US-0634641
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-539569/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 AA;
                                                                                                                                                                                                                                                                                                                                                        Lauwereys MJ,
Vlasuk GP;
                                                                                                                                                                                                                05-JUN-1995;
05-JUN-1995;
17-OCT-1995;
                                                                                            19-APR-1996;
              US5955294-A.
                                                    21-SEP-1999
                                                                                                                                                         18-OCT-1994;
05-JUN-1995;
                                                                                                                                                                                             3661-NUT-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
17-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present
                                                                                                                                                                                                                                                                                                                                          Bergum PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR91710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AceNAP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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Laroche YR;

Lauwereys' MJ,

Bergum PW;

Gaps

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62

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6 CGENEKYDSCGS-KECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD--CVCEEGFYRNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lauwereys N
Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bergum PW,
                                                                                                                                                                                                                AAY30419;
                                                                                                                                                 RESULT 14
                                                                                                                                                                    AAY30419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a nematode extracted anticoagulant protein (MAP). The protein has activity as an anticoagulant and/or serine protein in this protein contains at least one NAP domain which has selective inhibitory activity for factor VIIA/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIA/TF selective inhibitory activity. The method comprises determining the time to clotting an isolated by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo cativated partial thromboplastin time (aPT) assay and an ex vivo prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where a calculating a PT to aPTT prolongation ratio, where a ratio at least cone is indicative of factor VIIA/TF inhibitory activity. The method is useful for determining if a protein has factor VIIA/TF inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                             Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.6%; Score 212; DB 20; Length 190; 50.0%; Pred. No. 2.1e-12; ive 11; Mismatches 19; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bergum PW, Gansemans YGJ, Jespers LS, Laroche YR;
Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
Vlasuk GP;
                                                                                                                                                                                                                  Nematode extracted anticoagulant protein AceNAP4.
                                                                                                                   AAY30384 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Fig 7A; 197pp; English.
                    || ::||| ||||||
167 SCVESDDCEYDNMDFI 182
                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0634641.
94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
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                                                                                                                                                                                  (first entry)
 63 KCVSAEDCELDNMDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                Ancylostoma ceylanicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-539569/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ10441.
                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1996;
                                                                                                                                                                                15-NOV-1999
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05-JUN-1995
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                                                                                                                                                 AAY30384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                  AAY30384
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Gaps

8

Best Local Similarity 50.0 Matches 38; Conservative

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protein (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and apTT assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value for a can assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a adoubting of clotting time relative to a baseline clotting value, calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIII-YFF inhibitory activity. The method is useful for determining if a protein has factor VIIIa/TF inhibitory
Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a nematode extracted anticoagulant
                                                                                                                                                                                                                                                                                                              Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 86;
                                                                                                                                                                                                                                                                              Mature nematode extracted anticoagulant protein AcaNAP44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Columns 131-134; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.6%; Score 202;
                                                                                                                                                                         AAY30419 standard; Protein; 86 AA.
                                                                   167 SCVESDDCEYDNMDFI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
95WO-US13231.
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I, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0634641
                                                 63 KCVSAEDCELDNMDFI
                                                                                                                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-539569/45
                                                                                                                                                                                                                                                                                                                                                                     Ancylostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1996;
                                                                                                                                                                                                                                             15-NOV-1999
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05-JUN-1995;
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05-JUN-1995
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us-09-498-556c-59.rag

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                                                     9
                                                                   5 KCGPGERLDCANKKPCEPKCKIETSEEEDDDVEETDVRCLVRVCERPLKCICKDGYYRNK 64
                                                  S OCGENERYDSCGSKECDKKCKYDGVEEEDD--EEPNVPCLVRVCHQ--DCVCEEGFYRNK
                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanssens PEH, Jespers LS, Gansemans YGJ, Moyle M; ssens JHL, LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                        Nematode-extracted anticoagulant protein; AcaNAP44; blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -

    A. caninum nematode-extracted anticoagulant protein AcaNAP44.

 1 Similarity 47.4%; Pred. No. 8.3e-12; 37; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                        canine hookworm; thrombosis; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 16; 197pp; English.
                                                                                                                                                                                                                                    AAB15304 standard; Protein; 86 AA.
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65 KGECVTDDVCQEDFMEFI 82
                                                                                                                  61 DDKCVSAEDCELDNMDFI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0809455.
94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
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                                                                                                                                                                                                                                                                                                    19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lauwereys MJ, Standar JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         Ancyclostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-531359/48.
N-PSDB; AAA73379.
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nematode parasites.
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05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1999;
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18-OCT-1994;
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                                                                                                                                                                                                                                                                     AAB15304;
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41.6%; Score 202; DB 21; Length 86; 47.4%; Pred. No. 8.3e-12;

Query Match Best Local Similarity

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                                                  S KCGPGERLDCANKKPCEPKCKIETSEEEDDDVEETDVRCLVRVCERPLKCICKDGYYRNK 64
                               5 QCGENEXYDSCGSKECDXKCKYDGVEEEDD - - EEPNVPCLVRVCHQ - - DCVCEEGFYRNK
 Gaps
   4
22; Indels
Mismatches
                                                                                                                                                                   Search completed: December 8, 2003, 09:16:38 Job time : 114.545 secs
 15;
                                                                                           61 DDKCVSAEDCELDNMDFI 78
                                                                                                             :||::|::||:
65 KGECVTDDVCQEDFMEFI 82
 37; Conservative
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Sequence Sequence Sequence

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searched:

Sequence

Sequence

Sequence

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Sequence 59, Application US/08465380

Sequence 59, Application US/08465380

Sequence 59, Application US/08465380

APPLICANT: Cocide F. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yeas R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum

TITLE OF INVENTION: PROTIEN

TITLE OF INVENTION: PROTIEN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
US-08-465-380-49
US-08-480-478-54
US-08-486-397-49
US-08-486-399-25
US-08-466-399-49
US-08-461-965-25
US-08-461-965-49
US-08-461-965-49
US-08-634-641-25
US-08-634-641-25
US-09-249-471-25
US-09-249-471-25
US-09-249-472-25
US-09-249-472-25
US-09-249-472-25
US-09-249-472-25
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US-09-249-472-25
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US-09-249-472-25
US-09-249-472-25
                                                                                                                                                                                                                                                                                                        AL IGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: Unne 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213/ 30-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 84 amino acids TYPE: amino acid
    JUPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                 US-08-465-380-59
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                                                                                                                    (without alignments)
91.060 Million cell updates/sec
                                                                                                   December 8, 2003, 09:13:31 ; Search time 39.0303 Seconds
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1 KATMQCGENEKYDSCGSKEC.....VSAEDCELDNMDFIYPGTRN 84
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-644-1-59
US-09-249-471-59
US-09-249-451-59
US-09-249-451-59
US-09-249-461-59
US-09-249-461-59
US-09-249-461-59
US-09-249-473-59
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US-09-249-461-128
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US-09-249-473-128
US-08-465-380-25
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-08-326-110A-50
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S-08-634-641-59
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Result No.

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                                            100.0%; Score 486; DB 2; Length 84; 100.0%; Pred. No. 4e-43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Application US/08486397

Patent No. 586642

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yang R. Laroche, Laurent S. Jespers,
APPLICANT: Yang R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT;
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: Une 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                       61 DDKCVSAEDCELDNMDFIYPGTRN 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 84 amino acids
                                                                                          84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                  Best Local Similarity
Matches 84; Conserv
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JS-08-465-380-59
                                                 Query Match
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1 KATMÓCGENEKYDSCGSKECDKKCKYDGVEEBDDEEPNVPCLVRVCHQDCVCEGFFRNK 60
1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yea R. Larcohe, Laurent S. Jespers,
APPLICANT: Year R. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: NEMATODE.
CORRESPONDENCE 356
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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100.0%; Pred. No. 4e-43;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFFICATION NUMBER: US/326,110
FILING DATE: OCCODER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                                                                61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                        61 DDKCVSAEDCELDNMDFIYPGTRN 84
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US-08-486-399-59
                                                                                                                                                                                                                                                                                      Sequence 59, Application US/08486399
Patent No. 5866543
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Best Local Similarity 100.0
Matches 84; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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RESULT

1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60

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1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
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APPLICANT: Jesperc,
APPLICANT: Gansemans, Yannica APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: BLOLGADE
COMPUTER: BLOLGADE
SOFTWARE: WORD BELLE
SOFTWARE: WORD P.C. DOS 5.0
FILING DATE: April 19, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: October 18, 1994
ATTORNEY AND SOFTWARE
NAME: HTGRS SITZANNET.
                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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Patent No. 6040441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 84 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
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US-09-249-471-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 486; DB 2; Length 84; Best Local Similarity 100.0%; Pred. No. 4e-43; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                            APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN
WUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vlasuk, George P. Vlasuk
Stanssens, Patrick Eric Hugo
Mensens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1899-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DDKCVSAEDCELDNMDFIYPGTRN 84
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             Sequence 59, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Ancyclostoma caninum US-08-461-965-59
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Patent No. 5955294
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 84 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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61 DDKCVSAEDCELDNMDFIYPGTRN 84

GENERAL INFORMATION:

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APPLICANT: Vlasuk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yamnick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
TITLE OF INVENTION: NEMATOBE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATOBE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATOBE-EXTRACTED SERINE
TITLE OF INVENTION: NE
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: World Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
FILING DATE: World 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: Ottober 17, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/26,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,158
REGERENCE/DOCKET NUMBER: 216/270
FEBECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                Sequence 59, Application US/09249472
Patent No. 6046318
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INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 84 amino acida TYPE: amino acida TYPE: amino acida TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                    APPLICANT: Industry, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Juspers, Laurent Stephane
APPLICANT: Juspers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum. Peter W
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 631 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
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PILLING DATA:
PRILING DATA:
PRILING DATE:
PROR APPLICATION NUMBER:
PCIVUSS5/13231
APPLICATION NUMBER:
PCIVUSS5/13231
APPLICATION NUMBER:
PCIVUSS5/13231
APPLICATION NUMBER:
PCILING DATE:
APPLICATION NUMBER:
PLING DATE:
APPLICATION NUMBER:
PRICATOR TO SEQUENCE TO SEGUENCE TO SEGUEN
Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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100.0%; Score 486; DB 3; Length 84;

Query Match

1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEFNVPCLVRVCHQDCVCEEGFYRNK 60

61 DDKCVSAEDCELDNMDFIYPGTRN 84

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; ORGANISM: Ancyclostoma caninum US-09-249-472-59

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1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPUVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                             Query Match 100.0%; Score 486; DB 3; Length 84; Best Local Similarity 100.0%; Pred. No. 4e-43; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Atansens, Joris Hidda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves.Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Georges, Laurent Stephane
APPLICANT: Georges, Jannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATOBE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
MANDED OF INVENTION: PROFEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                61 DDKCVSAEDCELDNMDFIYPGTRN 84
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ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                             61 DDKCVSAEDCELDNMDFIYPGTRN
                                                                                                       Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/08809455 Patent No. 6090916
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APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 633 West Fifth Street
STREET: Suite 4700
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     ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancyclostoma
US-09-249-451-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                       1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                                 0; Gaps
Best Local Similarity 100.0%; Pred. No. 4e-43;
Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 815" Diskette, 1.44 Mb
MEDIUM TYPE: 810 TAGG
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/USS5/13231
                                                                                                                                                                        61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                       61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FC110959/1362
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Application US/09249451
Patent No. 6087487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INBIATOBE-ITILE OF INVENTION: INHIBITOR:
TITLE OF INVENTION: PROTEIN
MUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                          US-09-249-451-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILIGN DATE: April 17, 1997
FILIGN DATE: April 17/1595/13231
                                                                                                                                                                                                                                                                                                       LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM:
US-09-249-461-59
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APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Hessens, Joris Hilda Lieven
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Gansenns, Yven Rene
APPLICANT: Gansenns, Yannick Georges Jozef
APPLICANT: Gansenns, Yannick Georges Jozef
APPLICANT: Bergum, Peter M.
ITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
ITTLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEAN
ITLE OF INVENTION: NEMATODE-STRACTED SERINE
CORRESPONDENCES: 356
CORRESPONDENCES: 356
CORRESPONDENCES: 356
STREET: Suite 4700
CITY: LOS Angelon
CITY: LOS Angelon
                                                                                                                                                                                                                                                                                                     100.0%; Score 486; DB 3; Length 84; 100.0%; Pred. No. 4e-43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICKATION DATA:
PRICKATION NUMBER: 08/809,455
FILING DATE: APFILIT, 1997
APPLICATION NUMBER: PCT/NS95/13231
FILING DATE: OCTODER 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                 ) ORGANISM: Ancyclostoma caninum
US-08-809-455-59
  (213) 489-1600
                TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 84; Conservative
                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
TELEPHONE:
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1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vlasuk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: 10HIBITORS AND ANTICOAGULANT
TITLE OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 486; DB 3; Length 84; Best Local Similarity 100.0%; Pred. No. 4e-43; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZAANE I.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (57-3510
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DDKCVSAEDCELDNMDFIYPGTRN 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 486; DB 4; Length 84;
100.0%; Pred. No. 4e-43;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 128, Application US/08465380

Patent No. 5863894

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Pater W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT;
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
MUMBER OF SIQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: APRIL 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DDKCVSAEDCELDNMDFIYPGTRN 84
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ER: 216/270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 216/
TELECOMONICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
ITELEY: 67-3510
INFORMATION FOR SEQ
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
Best Local 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-465-380-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KATMOCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 486; DB 3; Length 84; Best Local Similarity 100.0%; Pred. No. 4e-43; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                       APPLICATION NUMBER: 08/486,399
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18,1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DDKCVSAEDCELDNMDFIYPGTRN 84
APPLICATION NUMBER: 08/10.,
APPLICATION NUMBER: 08/10.,
THE DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Ancyclostoma caninum US-09-249-448-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Application US/09249473 Patent No. 6534629
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-249-473-59
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1 KATMOCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 486; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 4.3e-43; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 128, Application US/08486397

Patent No. 586632

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Yves R. Larcche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,

APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Sail West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATE: 30
PLING DATE: 18 OCTOBER 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECHONNICATION INFORMATION:
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 DDKCVSAEDCELDNMDFIYPGTRN 91
                                                                                                                                                                                                                                                                  TELERAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 489-1600
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 KATMOCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-480-478-50

| Sequence 50, Application US/08480478
| Sequence 50, Application US/08480478
| PAPLICANT: B64009
| APPLICANT: HUGO STANSSENS; DORIS HILDA
| APPLICANT: LIEVEN MESSENS; MARC JOZEF
| APPLICANT: LAUWERRYS; YVES RENE LAROCHE;
| APPLICANT: LAUWERRYS; YVES RENE LAROCHE;
| APPLICANT: YANNICK GEORGES JOZEF
| APPLICANT: YANNICK GEORGES JOZEF
| APPLICANT: ANNICK GEORGES JOZEF
| APPLICANT: ANNICK GEORGES JOZEF
| APPLICANT: GINVENTION: COAGULANT PROTEIN
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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: JUME 5, 1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 213/268
TELECOMONICATION INFORMATION:
TELECHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acids
TYPE: amino acids
TOPPLOXY: linear
TOPPLOXY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DDKCVSAEDCELDNMDFIYPGTRN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 DDKCVSAEDCELDNMDFIYPGTRN 91
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US-08-465-380-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 813 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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Best Local Similarity
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Sequence:

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OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/09498272;
Publication No. US20030113890A1
GENERAL INFORMATION;
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Gansseman, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
. US-09-498-272-65

US-09-498-272-64

US-09-498-272-64

US-09-498-272-65

US-09-498-272-65

US-09-864-866-43

US-09-864-866-43

US-09-801-368-24

US-09-498-272-81

US-09-498-272-81

US-09-498-272-45

US-09-498-272-45

US-09-498-272-45

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US-09-498-272-46

US-09-498-272-46

US-09-498-272-46

US-09-498-272-46

US-09-925-302-855

US-09-925-302-855

US-09-913-718-16

US-09-913-718-16

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US-09-913-718-10

US-09-913-718-10

US-09-913-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10

US-09-813-718-10
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth (311te 4700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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86
86
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87
173
260
392
415
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471
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   TITLE
   Sequence 27, Appl
Sequence 24, Appl
Sequence 11215, A
Sequence 1934, Ap
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209.232 Million cell updates/sec
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Sequence 52,
Sequence 50,
                                                                            8, 2003, 09:18:46; Search time 6.2222 Seconds
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Sequence 4
Sequence 5
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(c) 1993 - 2003 Compugen Ltd.
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US-09-498-272-79
US-09-498-272-47
US-09-498-272-49
US-09-498-272-52
US-09-498-272-50
US-09-498-272-50
US-09-498-272-59
US-09-498-272-59
US-09-498-272-59
US-09-498-272-128
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Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                     Copyright
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Perfect score:
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Result Š.

Sequence 14, Appl Sequence 12, Appl Sequence 164, Appl Sequence 166, App Sequence 558, Appl Sequence 558, Appl Sequence 10, Appl

Sequence 2, Appli Sequence 171, App

Sequence Sequence

855, App 5, Appli 16, Appl 14, Appl 12, Appl

Sequence Sequence 1

Sequence 43, Sequence 855,

Sequence 4

Sequence 72, Ap Sequence 81, Ap Sequence 45609, Sequence 45, Sequence 46,

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

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TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INFILE OF INVENTIORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/09498272;
Publication No. US20030113890A1;
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; I
6.le+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                    FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 30,159
REGISTRATION NUMBER: 30,159
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUTCATION INPORMATION:
APPLICATION NUMBER: PCT/US95/13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 30; DB 100.0%; Pred. No. 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is an amino acid, provided that at least one Xaa is Glu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASP.
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                   FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TPDOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 71, Application US/09498272; Publication No. US20030113890A1; GENERAL INFORMATION; APPLICANT: Vlauk, George Phillip Stanssens, Doris Hilda Lieven Lauvereys, Marc Josef Laroche, Yves Rene Jespers, Laurent Stephane Jespers, Laurent Stephane Gansemans, Yamick Georges Jozef; Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                           NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30.158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTER.FSTICS:
LENGTH: 5 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEMATODE-EXTRACTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 30; DB 100.0%; Pred. No. 6.1 ive 0; Mismatches
             FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GFYRN 7
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Bergum, Peter W.
TITLE OF INVENTION: NEWANTODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/09498272;
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                           5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Ancyclostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-498-272-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 30; 100.0%; Pred. No.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
28;
                                                                                                                                                        APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                    OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                         APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 30; DB 100.0%; Pred. No. 28; Itive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
COMPUTER: 1BM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09498272
Publication No. US20030113890A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 GFYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GFYRN 7
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US-09-498-272-25
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Gaps
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Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 30; DB 11; Length 83; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY AGENT INCRMANTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT /
102.09-498-272-50
; Sequence 50, Application US/09498272
; Publication No. US20030113890A1
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                        OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04. Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Ancyclostoma duodena.
SEQUENCE DESCRIPTION: SEQ ID NO: 52
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                    COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                      STATE: California COUNTRY: U.S.A.
                                             CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFYRN 59
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BITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.8%; Score 30; DB 11; Length 82; 100.0%; Pred. No. 29; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
Standsens, Patrick Eric Hugo
Messens, Joris Hilds Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                        PADLICATION DAIRS.

PRICE APPLICATION NUMBER: PCT/US95/13231

RILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/46,965

RILING DATE: June 5, 1995

APPLICATION NUMBER: 08/46,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1994

ATTORNEY AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REGISTRATION NUMBER: 30,158

REGISTRATION NUMBER: 30,158

TELERCOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272 FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Ancyclostoma ceylanicum SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-498-272-52
; Sequence 52, Application US/09498272
; Publication No. US20030113890A1
                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                           ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserva
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51 GFYRN 55
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Gaps
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  TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
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30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: October 17, 1995

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486, 399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486, 397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465, 380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461, 965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461, 965

FILING DATE: June 5, 1996

APPLICATION NUMBER: 08/461, 965

FILING DATE: October 18, 1994

ATTORNEY/AGGNT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTATION NUMBER: 30, 186
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Peb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 216/270
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Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%; Score 30;
100.0%; Pred. No.
:ive 0; Mismatch
                                                                   NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSE: Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 84 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GFYRN 60
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US-09-498-272-59
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Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Ganssemane, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
                                                                                                                                                                       ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Ancyclostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 30;
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: October 18, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 84 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                  storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 GFYRN 60
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Gaps
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Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEWALTODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%; Score 30; DB 11; Length 89; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-200
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY AGENT: NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Ancyclostoma ceylanicum
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-498-272-128
; Sequence 128, Application US/09498272
; Publication No. US20030113890A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 89 amino acids TYPE: amino acid
                                                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                             Beigum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 84; 30;
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    Gansemans, Yannick Georges Jozef
Moyle, Matthew
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FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8%; Score 30;
100.0%; Pred. No.
:ive 0; Mismatcl
                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
*LENGTH: 84 amino acids
TYPE: amino acid
                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                    storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                      NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                             Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 GFYRN 59
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US-09-498-272-48
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93.8%; Score 30; DB 11; Length 102; 100.0%; Pred. No. 36; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                            Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-F6b-2000
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                         Stanssens, Patrick Bric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMË: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Ancyclostoma duodenale
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                         Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
     Sequence 27, Application US/09498272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 356
                                Publication No. US20030113890A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: Californía
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                       Bergum, Peter W.
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.8%; Score 30; DB 11; Length 91; Best Local Similarity 100.0%; Pred. No. 32; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                              Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICATION NUMBER: US/09/498,272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

FILING DATE: 04-Feb-2000

PRILING DATE: 04-Feb-2000

FILING DATE: 04-Feb-2000

FILING DATE: 04-Feb-2000

FILING DATE: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October: 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                             Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-09-498-272-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
APPLICANT: Vlasuk, George Phillip
                                                                           Lauwereys, Marc Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 128:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        storage
                                                                                                                                                                                                                                                                                                                                                                                                                   Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                             SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||
62 GFYRN 66
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74 GFYRN 78

RESULT 12 US-09-498-272-27

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) TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11215
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-877-1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GFYRN 66
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                                                                        RESULT 14
JS-10-156-761-11215
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US-09-764-877-1934
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                                                                                                                                                                                                                                                                                                                       Bergum, Peter W.
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                 APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREDICATION DATA:

PAPPLICATION NUMBER: US/09/498,272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

PAPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: June 5, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 316,270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Ancyclostoma ceylanicum SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
                                           ; Sequence 24, Application US/09498272; Publication No. US20030113890A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
RESULT 13
US-09-498-272-24
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Gaps

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Fatent No. US20020147140A1

Fatent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TILE OF INVENTION: WOUSER:

FILE REFERENCE: PCOOS

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper;

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1934

LINGTH: 138
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100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.8%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 40; Matches 5; Conservative 0; Mismatches
                                                              APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAXOSHI
APPLICANT: HATTORI WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-226
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11215
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 8, 2003, 09:34:03 Job time : 6.22222 secs
Sequence 11215, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-465-380-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELER: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
                                                                                                                                                                                                                                       US-08-465-380-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       (without alignments)
91.060 Million cell updates/sec
                                                          December 8, 2003, 09:13:31 ; Search time 3.25253 Seconds
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Sequence 4
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-08-634-641-70
S-09-249-471-70
S-09-249-471-70
S-08-249-451-70
S-08-249-461-70
S-09-249-461-70
S-09-249-461-70
S-09-249-473-70
S-08-465-380-79
S-08-466-397-79
S-08-466-397-79
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                                                                                                                                                                        328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                        Issued Patents AA:*
                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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32
1 XXGFYRN 7
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Match Length
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                                                                                                 Title:
Perfect score:
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US-08-461-965-47
US-08-634-641-47
US-09-249-472-47
US-09-249-451-47
US-08-809-455-47
US-08-249-473-47
US-09-249-473-47
US-09-249-473-47
US-08-465-380-45
US-08-466-397-25
US-08-486-397-25
US-08-486-397-25
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US-08-486-397-25
US-08-466-397-25
US-08-466-397-25
US-08-466-397-25
US-08-461-965-25
US-08-461-965-25
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Sequence 70. Application US/08465380

Fatent No. 5863894

GENERAL INFORMATION:
FAPLICANT:
FAPLICANT

ALIGNMENTS

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.

COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: Unne 5, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
ATTORNEY/AGENT IRFORMATION:
NAME: BIGGS, SUZANDE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUTCATION INFORMATION:
TELECHONE: (213) 489-1600

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amino acid
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                                                                                                                                                                                                                            Sequence 70, Application US/08486397
Facett No. 586542
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yeas R. Laroche, Laurent S. Jespers,
APPLICANT: Yean R. Laroche, Laurent S. Jespers,
APPLICANT: Peers W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT:
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%; Score 30; DB 2; Length 5; 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0; Indels
                  93.8%; Score 30; DB 2; Length 5; 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBET 18, 1994
ATTORNEY/AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 313/269
FILECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-486-399-70
; Sequence 70, Application US/08486399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-486-397-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERAX: (713) 955-0440
TELEXX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (213) 489-1600
Query Match
Best Local Similarity 100...
5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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1 GFYRN 5
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                                                                                                  GFYRN 7
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                                                                                                                                                                                                                        US-08-486-397-70
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PREPERTORY: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Li. Monnens, March J. Lawcercy,
APPLICANT: George P. L. Monnens, March S. Georges,
APPLICANT: Winnick G. J. Gansensins, Matthew Moyle,
APPLICANT: Got New Triple G. J. Gansensins, Matthew Moyle,
STREET: G. J. George F. Lith Street
STREET: G. J. George F. J. George F. J. George F. Lith G. George F. J. George
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TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%; Score 30; DB 2; Lv 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/634,641 FILING DATE: April 19, 1996 APPLICATION NUMBER: U5/08/634,641 APPLICATION NUMBER: PCT/US95/13231 FILING DATE: October 17, 1995 APPLICATION NUMBER: 08/486,399 FILING DATE: June 5, 1995 APPLICATION NUMBER: 08/486,397 FILING DATE: June 5, 1995 APPLICATION NUMBER: 08/465,380 FILING DATE: June 5, 1995 APPLICATION NUMBER: 08/46,397 APPLICATION NUMBER: 08/46,397 APPLICATION NUMBER: 08/46,397 APPLICATION NUMBER: 08/46,395 APPLICATION NUMBER: 08/46,396 APPLICATION NUMBER: 08/46,396 ATTONEY AGENT INFORMATION: NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 30,158 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
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ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.8
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GEYRN 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                    COMPUTER READABLE FORM:

MADIUM TYPE: 3." Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPatible
COMPUTER: IBM COMPatible
COMPUTER: Mord Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: US/08/461,965
FILING DATE: US/08/461,965
FILING DATE: US/08/461,965
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, USTANNE L.
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,128
TELEPHONE: (213) 499-1600
TELEPHONE: (213) 955-0440
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
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Mensens, Joris Hilda Lieven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 70, Application US/08634641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.8
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                              . Los Angeles
California
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                                                                            U.S.A.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-461-965-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-08-634-641-70
                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: SPOTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon
STREET: Suite 4700
                                                                 MEDDIUM TYPE: Storasys
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
FILING DATE: PRIOR APPLICATION NUMBER: 08/809,455
FILING DATE: APPLICATION NUMBER: 08/809,455
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTONNEY ACENT THYORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFREENCE/DOCKET NUMBER: 216/270
TELECHOMINICATION INPORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEST: 67-3510
INPORMATION FOR SEG ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70, Application US/09249451; Patent No. 6087487; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gespers, Laurent Stephane
APPLICANT: Bergum, Peter W.
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATOBE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.8%; Score 30; DB 3; Length 5; 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                     FILING DATE:

APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 08/809,455
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,1965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,1965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECPHONIS (213) 489-1600
TELEPHONIS (213) 955-0440
TELEPHONIS (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-249-472-70
; Sequence 70, Application US/09249472
; Patent No. 6446318
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laroche, Yves Rene
deppers, Laurent Stephane
Gansemans, Yamick Georges Jozef
Moyle, Matthew
                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: 810 Diskette, 1.44 Mb
MEDIUM TYPE: 810 DISKETTE, 1.45 DISKET, 1.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
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FRAGMENT TYPE: internal fragment
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                          Los Angeles
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                            COUNTRY:
   STREET:
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ENTION: NEMATODE-EXTRACTED SERINE PROTEASE
ENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PErfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
                                                                                                                                                                                                                                                                                                                                                          PRICATION DATA:

APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-809-455-70
; Sequence 70, Application US/08809455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 5 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NEW TITLE OF INVENTION: PROFILE OF INVENTION: PROFILE OF INVENTION: PROFILE OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-249-451-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.8%; Score 30; DB 3; Length 5; 100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanssens, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                PELLING DATE:
PRICK APPLICATION NUMBER: US/09/249/448
PRILING DATE:
PRILING DATE: APRIL 17, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: COCCODE: 17, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: CCCODE: 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
RECISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECPHONE: (213) 955-0440
                                                                                                                                                                                                         ZIF: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
                                                                    ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-249-473-70
; Sequence 70, Application US/09249473
; Patent No. 6534629
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 amino acids
TITLE OF INVENTION: PRO
NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vlaauk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                  PRILICATION NUMBER: 08/809,455
FILING DATE: April 17, 1995
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 316,1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 316,120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                ZIE: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 70, Application US/09249448
Parent No. 6121435
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                    Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                  U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFYRN 5
                                                                                            STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-249-448-70
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JECONE 197-79

Sequence 79, Application US/08486197

Sequence 79, Application US/08486197

SERENAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Oris H.L. Mensens, Marc J. Lauwereys,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT:

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
          TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SURUNCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Xaa in locations 1 and 2
INFORMATION: is an amino acid, provided
INFORMATION: that at least one Xaa is Glu or
INFORMATION: Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.8%; Score 30; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.5e+05; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: atcrage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amin.
                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GFYRN 7
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                     NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
                                                                                             NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 470
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTEN FRADABLE FORM:
MEDIUM TYPE: 315" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: 08/486,399
FILING DATE: OLODE 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/306,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/306,110
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/306,110
FILING DATE: JUNE 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERAK: (213) 955-0440
TELEK: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
APPLICANT: Bergum,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-249-473-70
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Query Match 93.8%; Score 30; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is an amino acid, provided
that at least one Xaa is Glu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa in locations 1 and 2 OTHER INFORMATION: is an amino acid, provide OTHER INFORMATION: that at least one Xaa is OTHER INFORMATION: Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 8, 2003, 09:20:29 Job time : 4.25253 secs
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLIASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 313/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1955-0440
TELEXX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
mono: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GFYRN 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yoes R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%; Score 30; DB 2; Length 7; 100.0%; Pred. No. 2.5e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa in locations 1 and 2
OTHER INFORMATION: is an amino acid, provided
OTHER INFORMATION: that at least one Xaa is Glu or
OTHER INFORMATION: Asp.
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: US/08/486,397
FILING DATE: October 18, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/ARDIT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 5; Conservative
                       California
: U.S.A.
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                                                    COUNTRY: U
ZIP: 90071
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US-08-486-399-79
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Gaps ö

0; Indels

Mature nematode ex Mature nematode ex Mature nematode ex Mature nematode ex A. caninum nematod Human digestive sy Mature nematode ex

Mature nematode ex A. ceylanicum nema A. ceylanicum nema

AcaNAPc2. Ancylos Nematode extracted Nematode extracted A. caninum nematod AcaNAP31. Ancylos Nematode extracted

A. duodenale nemat Nematode extracted A. ceylanicum nema Maize plastid targ Human musculoskele Novel human muscul

Human nervous syst Nematode extracted A. duodenale nemat

Mature nematode ex Mature nematode ex A. caninum nematod A. caninum nematod A. caninum nematod Mature nematode ex

AduNAP7. Ancylost Nematode extracted AcaNAP45. Ancylos AcaNAP47. Ancylos Nematode extracted Nematode extracted

Laroche YR;

Messens JHL, Lauwereys MJ,

Vlasuk GP, Stanssens PEH,

Result No.

6459789

OM protein

Run on:

Sequence:

Perfect

Searched:

Database

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AcaNAP; HpoNAP; NamNAP; AceNAP; AduNAP; anticoagulant; nematode-extracted anticoagulant protein; serine protease; nematode; thrombosis; parasitic worm.
                                                                                                                                                                                     ALIGNMENTS
             AAY30425
AAY30423
AAY30424
AAY30432
                                          AAY30421
AAR91701
AAY30393
AAY30454
AAB15346
                                                                                         AAY30398
AAB15292
AAY70530
                                                                                                             ABU13281
AAY30438
AAY30436
AAY30437
AAB15321
AAB15322
AAY30435
                                 AAB15317
AAM91998
                                                                                AAY30401
AAB15295
                                                                                                                                               AAR91713
AAY30388
                                                                      AAY30407
ABB14986
                                                                                                                                                             AAR91712
AAY30409
                                                                  AAR91709
                                                                                                        ABB03987
                                                                                                                                                                      AAY30410
                                                                                                                                                                                                            AAR91721 standard; Protein; 5 AA
                                                                                                                                                                                                                                                                                                                95US-0486399.
94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
 01000100010000110000110
                                                                                                                                                                                                                                                                                                       95WO-US13231.
                                                                                                                                                                                                                               (updated)
(first entry)
(CORV-) CORVAS INT INC
NAP subsequence.
                                                                                                                                                                                                                                                                                    WO9612021-A2
                                                                                                                                                                                                                                                                                                                     18-OCT-1994;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                       17-0CT-1995;
                                                                                                                                                                                                                               25-MAR-2003
17-NOV-1996
                                                                                                                                                                                                                                                                                             25-APR-1996,
                                                                                                                                                                                                                                                                                                                 05-JUN-1995
                                                                                                                                                                                                                                                                          Synthetic.
AAR91721;
NAP subsequence.
Nematode extracted
NAP domain fragmen
Mature nematode ex
A. caninum nematod
                                                                                                                                                                                                                                                                                                                     Nematode extracted
NAP domain fragmen
                                     (without alignments)
116.399 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                NAP subsequence,
                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            8, 2003, 09:13:30 ; Search time 9.54545 Seconds
                                                                                                                                                                                                                                                                                                       Description
                                                                                              1107863
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                            of hits satisfying chosen parameters:
                                                                                    1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    AAY30440
AAB15325
AAR91730
AAY30449
AAB15334
AAY30420
AAY30420
                                                                                                                                                                                                                                                                                                                AAR91721
                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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32
1 XXGFYRN 7
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Match Length
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WPI; 1999-539569/45.
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17-APR-1997;
18-OCT-1994;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-1999;
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                   05-JUN-1995;
17-OCT-1995;
05-JUN-1995;
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                                                                                                                                                                    Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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Matches
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                                                                                                                                                                                                                         activity, isolated from nemacodes, are useful to inhibit blood cocapilation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or in vivo diagnostic agents. The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concil levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may double the clotting time of human plasma in prothrombin time assays when present at 10-50 mMol, and double the clotting time of human c plasma in activated partial thrombin time assays when present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The anticoagulant proteins are pref. derived from Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligomosmoides polygyrus.

The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv., do not specifically inhibit the activation of factor VIIa in the absence of TF and do not specifically inhibit prothrombinase.

Proteins given in AAR91720-R91732 are preferred subsequences
                                                                               Proteins with anticoagulant and/or serine protease inhibitory activity - isolated from nematodes and useful to inhibit blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                              Proteins with anticoagulant and/or serine protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 17; Length 5; Pred. No. 9.3e+05;
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Bergum PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PI field.)
Moyle M,
                                                                                                                                                                    Claim 10; Page 144; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8%; Scc.
100.0%; Pred
0; N
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94US-0326110.
95US-0461965.
95US-0465380.
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Gansemans YGJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      generic NAP sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Local 5; Conserve
                                       WPI; 1996-222007/22
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Jespers LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1996;
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05-JUN-1995
                                                                                                                           coagulation
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AC AAY3
XX
DE NEME
XW
KW
NEME
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#X#X####X#X999999999999999999999
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The present sequence represents a nematode extracted anticoagulant protein (NAP) fragment. The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one and/or serine protease inhibitory activity for factor VIIa/TP.

The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TP selective inhibitory activity.

The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thrombollastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a cravit at least one is indicative of factor VIIa/TF inhibitory activity.

The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                          Laroche YR;
Stanssens PEH;
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100.0%; Pred. No. 9.3e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                          Jespers LS,
Moyle M, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 151; 197pp; English.
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94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
95WO-US13231.
                                                                                                                                                                                                                       Bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0249451.
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Les 5; Conservative
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05-JUN-1995;
18-OCT-1994;
05-JUN-1995;
                                            05-JUN-1995;
                                                                                                 Vlasuk GP,
Jespers LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY30449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY30449
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                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                     The present sequence is a fragment of the NAP domain (see AAB15347), which is found in all nematode-extracted anticoagulant proteins (NAPs). Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. They can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, perutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can also be used for this) or as diagnostic tests. The proteins can also be used for this) or as diagnostic tests. The proteins can also be used as vaccines against nematode parasites.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                     Lauwereys MJ, Stanssens PEH, Jespers LS, Gansemans YGJ, Moyle M; Bergum PW, Messens JHL, LaRoche YR, Vlasuk GP;
                                                                                                         New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Glu, Asp, OTHER
/note= "at least one of residue 1 or residue 2
is Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Glu, Asp, OTHER /note= "at least one of residue 1 or residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AcaNAP; HpoNAP; NamNAP; AceNAP; AduNAP; anticoagulant; nematode-extracted anticoagulant protein; serine protease; nematode; thrombosis; parasitic worm.
                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 30; DB 21; Length 5; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is Glu or Asp"
                                                                                                                                                  Claim 3; Column 285; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR91730 standard; Protein; 7 AA.
95US-0486397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
                              (CORV-) CORVAS INT INC.
                                                                                    WPI; 2000-531359/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 1
                                                                                                                                                                                                                                                                                                                             5 AA;
                                                                                                                                                                                                                                                                                                                                                                                           3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                               1 GFYRN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAP subsequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9612021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
17-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR91730;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91730
셤
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Proteins with anticoagulant and/or serine protease inhibitory activity, isolated from nematodes, are useful to inhibit blood cogulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or in vivo diagnostic agents. The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP conc. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may double the clotting time of human plasma in prothrombin time assays when present at 10-50 nMol, and double the clotting time of human plasma in activated partial thrombin time assays when present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                   Lauwereys MJ, Laroche YR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The anticoagulant proteins are pref. derived from Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligomosmoides polygyrus.

The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv. do not specifically inhibit the activation of factor VIIa in the absence of TF and on the specifically inhibit prothrombinase.

Proteins given in AAR91720-R91732 are preferred subsequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins with anticoagulant and/or serine protease inhibitory activity - isolated from nematodes and useful to inhibit blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematode extracted anticoagulant protein fragment.
                                                                                                                                                                                                                                                                                                                        Moyle M, Bergum PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; L
. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a generic NAP sequence. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 30; DB 100.0%; Pred. No. 9.3 Live 0; Mismatches
                                                                                                                                                                                                                                                                                   Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Page 147; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY30449 standard; Peptide; 7 AA.
95US-0486399.
94US-0326110.
95US-0461965.
                                                                                                                                                                                                                                                                                                                        Gansemans YGJ,
                                                                                                      95US-0465380
95US-0486397
                                                                                                                                                                                                                                                                                   Stanssens PEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-222007/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA;
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19-APR-1996;

19-APR-1996

US5955294-A

21-SEP-1999

05-JUN-1995; 17-OCT-1995;

05-JUN-1995 05-JUN-1995

05-JUN-1995

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The present sequence is a fragment of the NAP domain (see AAB15347), which is found in all nematode-extracted anticoagulant proteins (NAPs). Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. They can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an archerosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequences can also be used for this) or as disagnostic tests. The proteins can also be used sagainst nematode parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanssens PEH, Jespers LS, Gansemans YGJ, Moyle M; ssens JHL, LaRoche YR, Vlasuk GP;
                 /label= OTHER
/note= "one of these two residues must be either
Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%; Score 30; DB 21; Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature nematode extracted anticoagulant protein AcaNAP31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 9.3 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Column 286; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY30420 standard; Protein; 78 AA.
                                                                                                                                                                                                                                 95WO-US13231.
97US-0809455.
94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
                                                                                                                                                                                           99US-0249451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lauwereys MJ, Stanssens
Bergum PW, Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC.
Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-531359/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ancylostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||
GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA;
                                                                                                                                                                                             12-FEB-1999;
                                                                                                                                                                                                                                                         17-APR-1997;
18-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                              35-JUN-1995
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                                                                                                                                                   11-JUL-2000
                                                                                                                                                                                                                                       17-0CT-1995
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                                                                                                                                                                                                                                                                                                                        35-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PXSXXXXXXXXXXXXXXX
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a nematode extracted anticoagulant protein (NAP) fragment. The protein has activity as an anticoagulant and/or serine procease inhibitor. The protein contains at least one (NAP) damain which has selective inhibitory activity for factor VIIa/TE. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TE selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay, calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting and calculating a PT to aPTT prolongation ratio, where a cratic at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematode-extracted anticoagulant protein; NAP domain; blood clotting; canine hookworm; thrombosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 30; DB 20; Length 7; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 155; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB15334 standard; Peptide; 7 AA.
                                                                                                                        96US-0634641.
94US-0326110.
95US-0461965.
95US-0463380.
95US-0486397.
95WS-0486399.
                                                                                                                                                                                                                                                                                                                              bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                                                                    96US-0634641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAP domain fragment #11.
                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-539569/45.
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Best Local Similarity
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3 GFYRN 7
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Gaps

.; 0

Indels

Unidentified

Key

19-DEC-2000

#X8X#X#X#X#X

AAB15334;

RESULT 6 AAB15334

Seguence

Matches

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nematode-extracted anticognism in the proteins AcaNAP21, AcaNAP42 and AcaNAP46. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The proteins can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The proteins can also be used as a vaccine against nematode parasites.
                                                                                                                                                                                                                                                                                               PEH, Jespers LS, Gansemans YGJ, Moyle M;
LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                        New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence comprises the Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematode extracted anticoagulant protein AceNAP4d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core 30; DB 2
Pred. No. 52;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%; Score 30;
100.0%; Pred. No.
:ive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 16; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY30399 standard; Protein; 82 AA.
                                                                                                                                                                                                                                                                                               Stanssens PEH,
                                                                                                   97US-0809455.
94US-0326110.
95US-0461965.
                                         99US-0249451.
                                                                                                                                                                 95US-0465380
95US-0486397
                                                                                 95WO-US13231
                                                                                                                                                                                                           95US-0486399
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                                                                                                                                                                                                                                                                                                                Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ancylostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-531359/48.
N-PSDB; AAA73378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GFYRN 7
                                                                                                                                                                                                                                                                                               Lauwereys MJ,
Bergum PW, M
                                       12-FEB-1999;
11-JUL-2000
                                                                               17-OCT-1995;
17-APR-1997;
                                                                                                                       18-OCT-1994;
05-JUN-1995;
                                                                                                                                                                 05-JUN-1995;
                                                                                                                                                                                                           35-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a nematode extracted anticoagulant protein has activity as an anticoagulant and/or scrine protein (NAP). The protein has activity as an anticoagulant and/or scrine proteins inhibitory activity for factor VIIa/TF. The specification as selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (PT) assay; and an ex vivo activated partial thromboplastin time (apr) assay; alculating of clotting effected by the isolated protein in each of the PT and appra assay, where prolongation of clotting isolated protein in each of alevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to appropriation ratio, where a ratio at least cone is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematode-extracted anticoagulant protein; AcaNAP31; AcaNAP42; AcaNAP46; canine hookworm; blood clotting; thrombosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening an isolated protein for Nematode-extracted Anticoagulant
Protein domains

    A. caninum nematode-extracted anticoagulant protein AcaNAP31,42,46.

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                                                                                                                                                                                                                                                                                                                Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Columns 133-134; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB15305 standard; Protein; 78 AA.
                                                                                          96US-0634641.
94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
                                                                                                                                                                                                                                                                                             bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                                       96US-0634641
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Best Local Similarity
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54 GFYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 AA;
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                                                                                                                18-OCT-1994;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                     19-APR-1996;
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               21-SEP-1999
                                                                                                                                                                                                                        17-0CT-1995
                                                                                                                                                                                                    05-JUN-1995
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Gaps

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0; Indels

Sequence activity

RESULT 8 AAB15305

δ g 96US-0634641. 96US-0634641.

19-APR-1996; 19-APR-1996;

Ancyclostoma caninum.

US6087487-A.

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Nematode-extracted anticoagulant protein; AceNAP4d2; blood clotting; canine hookworm; thrombosis; vaccine.

    A. ceylanicum nematode-extracted anticoagulant protein AceNAP4d2 #1.

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97US-0809455.
94US-0326110.
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Best Local Similarity
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GFYRN 55
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17-APR-1997;
18-OCT-1994;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
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                                                                                                                         17-0CT-1995;
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AAB15293
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      THE SECTION OF THE SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitory. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification for for factor VIIa/TF selective inhibitory activity. The method comprises cateraning the time to clotting effected by a concentration of the isolated protein in an ex vivo protrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the act assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where calculating a pT to apTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
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Protein domains
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                                                                                                                                                                                                                                            Bergum PW, Gansemans YGJ, Jespers LS, Laroche YR;
Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%; Score 30; DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 111-112; 197pp; English
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      94US-0326110.
95US-0461965.
95US-0465380.
95US-0486399.
95WO-US13231.
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94US-0326110
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Best Local Similarity
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18-OCT-1994;
                                                                 05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
17-OCT-1995;
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protein (NAP). The protein has activity as an anticoagulant and/or serine protein challed to protein has activity as an anticoagulant and/or serine protein contains at least one NAP domain which can selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF. The specification of confirming the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay, and an ex vivo prolongation of clotting effected by the isolated protein in each of prolongation of clotting effected by the isolated protein in each of can assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where calculating a PT to aPTT prolongation there a ratio at least cone is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
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Protein domains
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100.0%; Pred. No. 55;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
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95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
95WO-US13231.
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Lauwereys MJ, Messens JHL,
Vlasuk GP;
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The present sequence is the Ancyclostoma ceylanicum nematode-extracted anticoagulant protein AcaNAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies in the latter instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
             Ξ
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             Moyle
                                                                                                   New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/FF.
         PEH, Jespers LS, Gansemans YGJ,
LaRoche YR, Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature nematode extracted anticoagulant protein AduNAP7d1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length
55;
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Moyle M, Stanssens PEH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine against nematode parasites.
                                                                                                                                                                           Disclosure, Fig 16; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30425 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940S-0325110
950S-0461965
950S-0465380,
950S-0486397,
950S-0486399,
95WO-US13231.
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Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0634641.
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                           Messens JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ancylostoma duodenale
                                                                WPI; 2000-531359/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GPYRN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GFYRN 7
         Lauwereys MJ,
Bergum PW, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the Ancyclostoma ceylanicum nematode-extracted anticoagulant protein AceNAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                    Gansemans YGJ, Moyle M;
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    A. ceylanicum nematode-extracted anticoagulant protein AceNAP4d2 #2.

                                                                                                                                                                                                                          New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains -
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55;
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                                                                                                                                  PEH, Jespers LS, Gansel
LaRoche YR, Vlasuk GP;
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93.8%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine against nematode parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB15307 standard; Protein; 82 AA.
                                                                                                                                    Stanssens PEH,
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
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94US-0326110.
95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
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                                                                                                                                                      Messens JHL,
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                                                                                             CORV-) CORVAS INT INC.
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                                                                                                                                                                                         WPI; 2000-531359/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AA;
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05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                  Lauwereys MJ,
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RESULT 12 AAB15307

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RESULT 15
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                                      The present sequence represents a nematode extracted anticoagulant protein (MAP). The protein has activity as an anticoagulant and/or serine protein in the protein contains at least one NAP domain which has selective inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIA/TF specification describes a method for screening an isolated protein at least one domain for factor VIIA/TF selective inhibitory activity. The method comprises determining the time to clotting an isolated protein at an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPT) assay, and an ex vivo prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where a calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIA/TF inhibitory activity. The method is useful for determining if a protein has factor VIIA/TF inhibitory
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                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                        93.8%; Score 30; DB 20; Length 83; 100.0%; Pred. No. 55; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laroche YR;
Stanssens PEH
                     Disclosure; Columns 137-138; 197pp; English.
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Moyle M,
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95US-0461965.
95US-0465380.
95US-0486397.
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Lauwereys MJ, Messens JHL,
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                        55 GFYRN 59
                                                                                                                                                                                                                                                     83 AA;
                                                                                                                                                                                                                                                                                                                   GFYRN 7
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                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                        Query Match
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The present sequence represents a nematode extracted anticoagulant protein has activity as an anticoagulant and/or serine protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one MAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the solated protein in an ex vivo prothrombin time (PT) assay and an ex vivo prothrombin time (PT) assay and an ex vivo prothrombin time (PT) assay and an ex vivo prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold clevation of clotting time relative to a baseline clotting value, where a doubling of clotting time relative to a baseline clotting value, where calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory
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Protein domains
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Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2
Disclosure; Columns 135-136; 197pp; English
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95US-0461965.
95US-0465380.
95US-0486397.
95US-0486399.
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AA;
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05-JUN-1995;
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Matches
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Disclosure; Columns 135-138; 197pp; English.

The present sequence represents a nematode extracted anticoagulant protein (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification can selective inhibitory activity. The specification of for factor VIIa/TF selective inhibitory activity. The specification of for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (PT) assay and an ex vivo activated partial thromboplastin time (PT) assay, and ex vivo cativated partial thromboplastin time (PT) assay, and the vivo each assay, where prolongation of clotting is calculating of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least cone is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory

Sequence 84 AA;

0; Gaps DB 20; Length 84; 56; 0; Indels Query Match 93.8%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 56; Matches 5; Conservative 0; Mismatches

3 GFYRN 7

||||| 56 GFYRN 60

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Search completed: December 8, 2003, 09:16:39 Job time : 10.5455 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 8, 2003, 09:13:30 ; Search time 1.83838 Seconds (without alignments) 179.063 Million cell updates/sec Run on:

US-09-498-556C-79 32

1 XXGFYRN 7 Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9z2do mus musculu	mycc			P46303 micrococcus	Q8ply7 xanthomonas		yersinia			Q92rl0 rhizobium m	P32921 mus musculu	_	P34651 caenorhabdi	P51612 mus musculu	Q01831 homo sapien					P57606 buchnera ap			Q8k9n0 buchnera ap			P76046 escherichia		æ	ω	~	Q9jhz2 mus musculu	P58366 rattus norv
SUMMARIES		MTR3 MOUSE	HPRT_MYCGE	HPRT MYCPN	END3_MYCTU	UVEN_MICLU	SERC_XANAC	SERC_XANCP	SERC_YERPE	SERC_XYLFA	SERC_RALSO	PUR2_RHIME	SYW_MOUSE	TYRO MOUSE	YOTS CAEEL	XPC_MOUSE	XPC_HUMAN	PDRA_YEAST	RL32_BORBU	YAJF_LACLA	KAD_CHLTE	DEOD_BUCAI	YF35_METJA	SOLR_CLOAB	K6PF_BUCAP	YD17_ARCFU	Y613_METJA	YCJX_ECOLI		YALS_SCHPO	SYW_BOVIN	SYW_RABIT	ANKH MOUSE	ANKH_RAT
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de	Query Match		93.8				93.8			•	•	93.8	93.8	93.8	93.8	93.8	93.8	93.8	84.4	84.4	84.4	84.4	84.4	. 84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4
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RESULT 2
HERT MYCGE
1D HPRT WYCGE STANDARD; PRT; 175 AA. AC B4756;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

||||| 105 GFYRN 109 3 GFYRN 7

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P12944 desulfovibr Q8zwk4 pyrobaculum Q03185 giardia lam P21849 giardia lam Q9554 fowlpox vir P11894 pisum sativ P25864 arabidopsis Q9cjb5 lactococcus P73715 syneochocyt Q9cb92 mycobacteri Q9cb92 etreptococcus Q97pp6 streptococcus	AA	uence update) otation update) (Fragment). Craniata; Vertebrata; Buteleostomi; Sciprognathi: Muriane: Murinae:	Tentler D., Kretz C., Dahl N., lual specificity phosphatase	-i - FUNCTION: NOT KNOWN, COULD BE A TYROSINE-PHOSPHATASEi - SIMILARITY: BELONGS TO THE MYOTUBULARIN-LIKE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).	NL. Nb. 18B98 CRC64; 1; Length 121; 0; Indels 0; Gaps
PHNL DESCI SYT PYRAE TS11 GIALA TSA4-GIALA V179-FOWPV RK9-FRATH YA1F LACLA END3-SYNY3 END3-MYCLE YQAC LACLA	ALIGNMENTS PRT; 121	Created) Last sequence update) Last annotation update) rotein 3 (Fragment). ordata; Craniata; Verte	9736772; Buj-Bello A., Tent myotubularin dual 712(1998).	FUNCTION: NOT KNOWN, COULD BE A TYROSINE-PHOSPHATASI SIMILARITY: BELONGS TO THE MYOTUBULARIN-LIKE FAMILY SWISS-PROT entry is copyright. It is produced throu- ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no re- by non-profit institutions as long as its contes- fited and this statement is not removed. Usage by Ities requires a license agreement (See http://www.is	sph ATA ATA ATA ATA ATA
84.4 550 1 84.4 667 1 84.4 667 1 84.4 713 1 81.2 91 1 81.2 218 1 81.2 218 1 81.2 218 1 81.2 245 1 81.2 245 1 81.2 245 1	STANDARD;		NCCHITAXID=10090; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-98409499; PubMed-9736772; Laporte J., Blondeau F., Buj-Bello A., Mandel JL.; "Characterization of the myotubularin d gene family from yeast to human."; Hum. Mol. Genet. 7:1703-1712(1998).	-! - FUNCTION: NOT KNOWN, COULD BE A TYR -! - SIMILARITY: BELONGS TO THE MYOTUBUL This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the European Bioinformatics Institute. Use by non-profit institutions as lo modified and this statement is not remo entities requires a license agreement (or send an email to license@isb.sib.ch)	81; AA 1552; R00038 0383; 0056; 1 21 AA 1 1arity
334 335 337 337 338 338 338 339 44 44 45 45 45 45 45 45	JT 1 MOUSE MTR3 MOUSE	Q922D0; 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 41, MyCubularin-related i MyEuxia. (Mouse). Mus musculus (Mouse). Rukaryota, Metazoa; Cf Mammalia: Eutheria: R	NCBI_TAXID=10090; [1] SEQUENCE FROM N.A. MEDLINE=98409499; Laporte J., Blonde Mandel JL.; Mcharacterization gene family from y Hum. Mol. Genet. 7	-!- FUNCTION -!- SIMILARI -!- SIMILARI This SUNSS-P between the European the European modified and entities req	EMBL, AF0738 MGD; MGI:192 InterPro; 1P PROSITE; PSD Hydrolase. NON TER SEQUENCE 1 Query Match Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mucleic Acids Res. 24:4420-4449(1996).
-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
alpha-D-ribose 1-diphosphate.
-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
                     01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI _TaxID=2104;
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PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyase).
NTH OR RV3674C OR MT3775 OR MTV025.022C.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                             Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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12;
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MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Purine salvage.
-!- SUBCELDLAR LOCATION: Cytoplasmic.
-!- SUBLIARILY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005904; Hxn_phspho_trans.
InterPro; IPR002375; Pr/py_rp_transf.
InterPro; IPR000836; PRTransferase.
Pfam; PP00156; Pribosyltran; 1.
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-D-ribose 1-diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000018; AAB95818.1; -. PIR; S73496; S73496.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
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069642;
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END3_MYCTU
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                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAILE-96026346; PubMed=756993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fleischmann J.L., Weidmann J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

The minimal gene complement of Mycoplasma genitalium.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 175:7918-7930 (1993).
-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
alpha-D-ribose 1-diphosphate.
-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
alpha-D-ribose 1-diphosphate.
-!- PATHMAY: Purine salvage.
-!- PATHMAY: Purine salvage.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
PHOSPHORIBOSYLTRANSFERASE FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
28-FEB-2003 (Rel. 41, Last annotation update)
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
(HGPRTase).
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                                                                                      Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRPAMB; TIGR01203; HGPRTase; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 1; Length 175;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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97 97 MAGNESIUM (BY SIMILARITY).
175 AA; 19759 MW; 9647332FFF3E18E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 AA
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InterPro; IPR002375; Pr/py rp transf.
InterPro; IPR000836; PRTransferase.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 9-98 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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                                                                                                                                 NCBI_TaxID=2097;
                                                                   HPT OR MG458.
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ID HERT MYCEN
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Gaps

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RESULT 3

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A InterPro; IRRU02.2

JR InterPro; IRRU0575; Nt...

DR Ffam; PF00633; HHH; 1.

DR SWART; SW00525; FES; 1.

DR TIGRRAMs; TIGNO1093; nth; 1.

DR PROSITE; PS01764; ENDONUCLEASE III 2; 1.

DR PROSITE; PS01155; ENDONUCLEASE III 2; 1.

DR PROSITE; PS00764; ENDONUCLEASE Multifunctional enzyme; DNA repair; Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair; APG-45; Complete protecmending in Proceedings of the Sumitarity.

198 198 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

IRON-SULFUR (4FE-4S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINS-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann, DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Folomay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                        MEDLINE-98255987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigleneier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL022121; CAA17996.1; ALT INIT.
EMBL; AE007175; AAK48142.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist; Rv3674c; ...
InterPro; IPR001265; Endo 3c.
InterPro; IPR004015; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003651; FeS_bind.
InterPro; IPR00445; HhH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P20625; 2ABK.
NCBI_TaxID=1773;
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                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ultraviolet N-glycosylase/AP lyase (UV-endonuclease) (Pyrimidine dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piersen C.E., Prince M.A., Augustine M.L., Dodson M.L., Lloyd R.S.;
"Purification and cloning of Micrococcus luteus ultraviolet
endonuclease, an N-glycosylase/abasic lyase that proceeds via an
imino enzyme-DNA intermediate.";
J. Biol. Chem. 270:23475-23484(1995).
- FUNCTION: HAS BOTH, AN APURINIC AND/OR APYRIMIDINIC ENDONUCLEASE
- FUNCTION: HAS DONH, ACTYCOSYLASE ACTIVITY. INITIATES REPAIR AT
CIS.SYN PYRIMIDINE DIMERS. PROCEEDS VIA AN IMINO ENZYME:DNA
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANDOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN CODONS FOR GLY-268 AND ALA-270. TWO FORMS OF 31 kDA AND 32 kDA HAVE BEEN DETECTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UV ENDONUCLEASE 31 kDa FORM.
UV ENDONUCLEASE 32 kDa FORM (PROBABLE).
     IRON-SULFUR (4FE-4S) (BY SIMILARITY)
                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Micrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGR01083; nth; 1.

PROSITE; PS00764; ENDONUCLEASE III_1; 1.

PROSITE; PS01155; ENDONUCLEASE III_2; 1.

Hydrolase; Nuclease; Endonuclease; DNA repair; Glycosidase;
                                                                                     Length 245;
  214 IRUN-SUMFUN 1112 27030 MW; 2B6D16195DD090DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                     DB 1;
16;
                                                                 93.8%; Scor.
100.0%; Pred. No. 10.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003265; Endo_3c.
Interpro; IPR004035; EndoIII_FCL.
Interpro; IPR004036; EndoIII_HhH.
Interpro; IPR0040365; Fes bind.
Interpro; IPR000445; HhH.
Interpro; IPR003583; HHH.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U22181; AAA86508.1; ALT_TERM.
HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN≂ATCC 4698;
MEDLINE=96007490; PubMed=7559510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
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Pfam; PF00633; HHH; 1.
SMART; SM00478; ENDO3C; 1.
SMART; SM00525; PES; 1.
SMART; SM00525; HHH; 1.
                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
214 2
245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iron-sulfur; 4Fe-4S
CHAIN 1
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                       |||||
91 GFYRN 95
                                                                                                                                                                                                   3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylase).
                                                                                                                                                                                                                                                                                                                                                 RESULT 5
UVEN_MICLU
ID UVEN_MICLU
AC P46303;
     METAL
SEQUENCE
                                                                                                                                                 Matches
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us-09-498-556c-79.rsp

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Q8PA97:
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RE SEQUENCE FROM N.A.

RE STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

RA Rateuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Takita M.A., Truffi D., Tsai S.M., White F.F.,

RA Schubal J.C., Kitajima J.P.;

RA Setubal J.C., Kitajima J.P.;

RA Setubal J.C., Kitajima J.P.;

RA Norst specificities of two Xanthomonas pathogens with differing and the perpendent of the genomes of two Xanthomonas pathogens with differing and the perpendent of the secondent of the seco
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                                                                                                                                                  ö
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULÂR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
               SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphonooxypyruvate + L-glutamate.
COFACTOR: Pyridoxal phosphate (By similarity).
PATHWAY: Required both in major phosphorylated pathway
biosynthesis and in the biosynthesis of pyridoxine (By
                                                                                                              Score 30; DB 1; Length 279;
                                                                                                                                                  0; Indels
203 203 IRON-SULFUR (4FE-4S) (BY S
210 210 IRON-SULFUR (4FE-4S) (BY S
213 213 IRON-SULFUR (4FE-4S) (BY S
219 219 IRON-SULFUR (4FE-4S) (BY S
279 AA, 30469 MW; C385369A1827C005 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Phosphoserine aminotransferase (BC 2.6.1.52) (PSAT)
                                                                                                                                                                                                                                                                                                                                                      [5-SEP-2003 (Rel. 42, Created)
[5-SEP-2003 (Rel. 42, Last sequence update)
[5-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                             100.0%; Pred. No. 19; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                     361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00160; -; 1.
InterPro; IPR0001923, AminotransfV.
InterPro; IPR003248; Peer amintransf.
Pfam; PF00266; aminotran_5; 1.
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011797; AAM36516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                                                                              93.8%;
                                                                                          Ouery Match
Best Local Similarity luv...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aminotransferases
                                                                                                                                                                                                                      95 GFYRN 99
                                                                                                                                                                                     3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                 SERC OR XAC1648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                        15-SEP-2003
                                                                                                                                                                                                                                                                                                                   SERC XANAC
QBPLY7;
                                                      METAL
SEQUENCE
                                      METAL
                                                                                                                                                                                                                                                                                                 SERC_XANAC
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=ATCC 33913 / NCPPB 528;

XX MEDLINE=20202145; PubMed=12024217;

XX Ga Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F.C. Ciapina L.P.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F.C. Ciapina L.P.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratisuyama A.M., Xishi L.T., Lette R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Maidanis J.M., Menck C.P., Mylyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okuru V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Tarkta M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Stindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

T. Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Nature 417:459-463(2002).
-!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-phosphonoxypyruvate + L-glutamate.
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Required both in major phosphorylated pathway of serine biosynthesis and in the biosynthesis of pyridoxine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
                            TIGREPANS; TIGRO1364; BETC 1; 1.
PROSITE; PSO0595; AA TRANSFER CLASS 5; 1.
Serine biosynthesis; Pyridoxine biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate; Complete protecome. BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                            DB 1; Length 361;
24;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                       75EC2B319C493982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
SERC OR XCCIS89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AA.
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                 93.8%; Score 30; 100.0%; Pred. No.
ProDom; PD001544; Pser_amintransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE012260; AAM40884.1; -.
HAMAP; MF 00160; -; 1.
InterPro; IPR000192; AminotransfV.
                                                                                                                                                                                               BINDING 196 196 P
SEQUENCE 361 AA; 38680 MW;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.00
Trahes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aminotransferases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=340;
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EMBL; AJ414148; CAC90218.1; -. EMBL; AE013881; AAM86336.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xylella fastidiosa.
                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                              283 GFYRN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERC OR XF2326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=9a5c;
                                                                                                                                                                                                                                                                                                                                                                                                      SERC XYLFA
                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna W.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CO-92 / Biovar Orientalis;
MEDINEs-1470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Ferzinia pestis, the causative agent of plague.";
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphonooxypyruvate + L-glutamate.
--- COFACTOR: Pyridoxal phosphate (By similarity).
--- PATHWAY: Required both in major phosphorylated pathway of serine blosynthesis and in the blosynthesis of pyridoxine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULĀR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
InterPro; IPR003248; rbet_will.

Pfam; PF00266; aminotran 5; 1.

Probom; PD001544; Pser_amintransf; 1.

TIGRFAMs; TIGRO1364; serC 1; 1.

PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.

PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.

Serine blosynthesis; Pyridoxine blosynthesis; Transferase;
Aminotransferase; Pyridoxal phosphate; Complete proteome.

Aminotransferase; Pyridoxal phosphate; Complete SIMILARITY)

PROSITE: ABMINARITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate =
                                                                                                                                                 DB 1; Length 361;
                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
                                                                                                                                                                Pred. No. 24;
                                                                                                                                                                                                                                                                                                               361 AA.
                                                                                                                                              93.8%; Score 30; DB 100.0%; Pred. No. 24; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                SERC OR YP01389 OR Y2784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:523-527(2001).
                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aminotransferases.
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                           283 GFYRN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                        3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                            SERC YERPE
Q8ZGB4;
                                                                                                                                                                                                                                                                                           SERC_YERPE
   SO F KW W D R S
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RESULT 11
PUR2_RHIME
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                                                                                                                                                                                                                                                                                                                                                                                 R BMB1; ARUNAUS,

R HSPP; P23721; 1BJN.

R HSSP; P23721; 1BJN.

R HAMAP; MF_00160; -; 1.

R InterPro; 1PR001924; Pser amintransf.

Prodom; P000154; Pser amintransf.

R PROSITE; PS00595; AA_TRANSFER CLASS 5; FALSE_NEG.

R Mainotransferase; Pyridoxal phosphate; Complete proteome.

R Mainotransferase; Pyridoxal phosphate; Complete proteome.

PYRLDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of serine
PATHWAY: Required both in major phosphorylated pathway of serine biosynthesis and in the biosynthesis of pyridoxine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULĂR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
aminotransferases.
                                                                      SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 0-phospho-L-serine·+ 2-oxoglutarate = 3-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphonooxypyruvate + L-glutamate.
COFACTOR: Pyridoxal phosphate (By sinilarity).
PATHWAY: Required both in major phosphorylated pathway
biosynthesis and in the biosynthesis of pyridoxine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%; Score 30; DB 1; Length 362; 100.0%; Pred. No. 24; 1.1.00.0%; Pred. No. 24; 1.1.00 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
SERC OR RSCO903 OR RS04512.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004043; AAF85125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 5; Conservative
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                                                                                                                           aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 GFYRN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
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QBYOZO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Glycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-!- CATALYTIC ACTIVITY: ATP + 5-phospho-D-ribosylamine + glycine = -+ phosphate + N(1)-(5-phospho-D-ribosyl)glycinamide.

-!- PATHWAY: De novo purine biosynthesis; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinami ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)
PURD OR RO0858 OR SWC00933.
Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00160; -; 1.

InterPro; IPR00192; Aminotransfv.

InterPro; PR00248; Pser amintransf.

Pfam; PP0026; aminotran 5; 1.

ProDom; PD00154; Pser amintransf; 1.

TIGRFAMS; TIGR01364; SerC 1; 1.

PROSITE; PS00055; AA TRANSFER CLASS 5; FALSE NEG.

Serine biosynthesis; Pyridoxine biosynthesis; Transferase; Aminotransferase; Pyridoxine biosynthesis; Pradoxine biosynthesis; Pyridoxine biosynthesis; Pyridoxine biosynthesis; Transferase; BINDING 214 214 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%; Score 30; DB 1; Length 378;
100.0%; Pred. No. 25;
ive 0; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 378 AA; 41860 MW; D4CA356D9098E97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AA.
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                                                                                                                                                                                                                                                                                                                     EMBL; AL646061; CAD14605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guery Match
Bost Local Similarity 100.00
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 GFYRN 304
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VARSPLIC
                                                                                                                  SEQUENCE
                                                                                                                                          Query Match
                                                    DOMAIN
SITE
                                                                                                                                                                                                                                                                        TYRO_MOUSE
                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

MEDLINE=95018226; PubMed=7932716;
Pajor B., Sarger C., Bonnet J., Garret M.;
Pajor B., Sarger I., Bonnet J., Garret M.;
An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells.";
J. Mol. Biol. 242:599-603(1994).
-!-CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!-SUBUNIT: Homodimer (By similarity).
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1; Synonyms=Long;
IsoId=P32921-1; Sequence=Displayed;
Name=2; Synonyms=Short;
IsoId=P32921-2; Sequence=VSP 006313;
-!- TISSUB SPECIFICITY: Isoform 2 Is widely expressed, isoform 1 is found only in embryonic stem cells.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
-!- SIMILARITY: Contains 1 WHEP-TRS domain.
                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                            .
0
                                                                                                              93.8%; Score 30; DB 1; Length 423; 100.0%; Pred. No. 28; 0; Indels ive 0; Mismatches 0; Indels
        Pfam; PF02842; GARS B; 1.
Pfam; PF02842; GARS C; 1.
Pfam; PF02844; GARS N; 1.
TIGREAMS; TIGR00877; Purb; 1.
PROSITE; PS00184; GARS; 1.
Purine biosynthesis; Ligase; Complete proteome.
SEQUENCE 423 AA; 44324 MW; 5E65E13B606D204B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                         481 AA.
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MGD; MGI:104630; Wars.
InterPro; IPR002305; FRNA-synt 1b.
InterPro; IPR001412; FRNA-synt_I.
InterPro; IPR001412; TRNA-synt_I.
InterPro; IPR001306; Trp FRNA-synt_I.
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00579; tRNA-synt_lb; 1.
Pfam; PF00458; WHEP-TRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1039; TRNASYNTHTRP.
TIGRFAMS; TIGR00233; trpS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X69656; CAA49347.1; -. EMBL; X69657; CAA49348.1; -.
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                         407 GFYRN 411
                                                                                                                                                                  3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                               WARS OR WRS.
                                                                                                                                                                                                                                                        SYW MOUSE
                                                                                                                Query Match
                                                                                                                                                                                                                               RESULT 12
SYW_MOUSE
SYNERS
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PROSITE; PS00178; AA TRNA LIGASE_I; 1.
PROSITE; PS00762; WHEP TRS; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                    Gaps
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Yamamoto H., Takeuchi S., Kudo T., Makino K., Nakata A., Shinoda T.,
Takeuchi T.;
"Cloning and sequencing of mouse tyrosinase cDNA.";
Jpn. J. Genet. 62:271-274(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
(Albino locus protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kwon B.S., Wakulchik M., Haq A.K., Halaban R., Kestler D.; "Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its gene expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89030636; PubMed=3141148;
Mueller G., Ruppert S., Schmid B., Schuetz G.;
"Functional analysis of alternatively spliced tyrosinase gene
                                                                                                                                                                                                                                                                                  Score 30; DB 1; Length 481;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                481 AA; 54282 MW; B05A452C08074F52 CRC64;
                                                                                                                           "HIGH" REGION.
"KMSKS" REGION.
Missing (in isoform 2).
/FTId=VSP_006313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 153:1301-1309(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Himalayan;
MEDLINE=89273644; PubMed=2567165;
Kwon B.S., Halaban R., Chintamaneni C.;
"Molecular basis of mouse Himalayan mutation.";
Biochem. Biophys. Res. Commun. 161:252-260(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 159:848-853 (1989)
                                                                                                                                                                                                                                                                                                            Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 AA
                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                         WHEP-TRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=88268910; PubMed=3134020;
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SEQUENCE OF 1-273 FROM N.A.
MEDLINE=90212084; PubMed=2517217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Created)
01-AUG-1990 (Rel. 15, Last seq
                                                                                                                                                                                                                                                                                  93.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 7:2723-2730(1988).
                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                    68
                                                                                                                                                                           481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   250 GFYRN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                      23
168
353
476
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CARBOHYD
                                                                                                  VARIANT
VARIANT
                                                                                                                                                               CONFLICT
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                                                                                                                                            VARIANT
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YOTS CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                     tyrosinase gene into mice.";
EMBO J. 9:2819-2826(1990).
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE PORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
COMPOUNDS: CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
INDOLE-5,6 QUINONE.
-!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOPAGUINONE + H(2)O.

COACTON: Binds 2 copper ions per subunit.

SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.

DISEASE: DEFECTS IN TYR RESULT IN VARIOUS FORMS OF ALBINISM.

HIMALAYAN STRAIN TYROSINASE IS TEMPERATURE-SENSITIVE.

SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.

CAUTION: REF. 4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.
Yamamoto H., Takeuchi S., Kudo T., Sato C., Takeuchi T.; "Melanin production in cultured albino melanocytes transfected with mouse tyrosinase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
POLY-LYS.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                        MEDLINE=90249393; PubMed=2110899;
Shibahara S., Okinaga S., Tomita Y., Takeda A., Yamamoto H., Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine-->serine substitution at position 85."; Eur. J. Biochem. 189:455-461(1990).
                                                                                                                                                                                                                                                                                                        MEDLINE=90360993; PubMed=2118105; Besrann F. Xuppert S., Hummler E., Bosch F.X., Mueller G., Ruether U., Schuetz G.; "Rescue of the albino phenotype by introduction of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUMENAL, MELANOSOME (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYROSINASE
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                                                          Jpn. J. Genet. 64:121-135(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D00440; BAA00341.1; -. EMBL; M20234; AAA40516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X12782, CAA31273.11, --
EMBL, M24560, AAA40517.11, --
EMBL, D00131, BAA00079.11, --
EMBL, X51743, CAA36033.11, --
EMBL, D00439, BAA00340.11, --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M26729; AAA37806.1; -.
                                                                                                                                                                                                                                                                                     VARIANT CHINCHILLA MICE.
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4476
4976
533
1180
202
201
201
367
367
508
86
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PIR; A27711; YRMSCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:98880;
                                                                                                  VARIANT ALBINO.
                                                                                                                                                                                    Takeuchi T.;
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DOMAIN
CARBOHYD
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                       ASRIWPWLLGAALVGAVIAAALSGL -> GQSYLAMASWGS
TGGSCCCGSLWA (IN REF. 5).
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favelb A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Saith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                      C -> S (IN ALBINO MICE).
H -> R (IN HIMALAYAN STRAIN).
A -> T (IN CHINCHILLA MICE).
M -> Q (IN REF. 2).
C -> Q (IN REF. 2).
V -> G (IN REF. 3).
V -> G (IN REF. 3).
ASPLYGIAD -> LFEHWOCG (IN REF. 5).
MISSING (IN REF. 5).
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                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 533; 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              533 MISSING (IN REF. 5)
60648 MW; 4B711312DDB6F7D1 CRC64;
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Wormbep; ZK632.5; CE00422.
Hypotherical protein.
SEQUENCE 824 AA; 95726 MW; 05074058F5B73919 CRC64;
                                                    (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein ZK632.5 in chromosome III.
ZK632.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 30; DB 100.0%; Pred. No. 36; Live 0; Mismatches
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 GFYRN 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GFYRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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P34651;
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                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lacking XPC.";
Nature 377:162-165(1995).
-!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
-!- SUBUNIT: HETERODIMER OF A 125 kDa SUBUNIT (P125) AND OF A
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96184849; PubMed=8604333;
Li L., Peterson C., Legerski R.;
"Sequence of the mouse XPC cDNA and genomic structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/Sv;

BEDLINES-29405469; PubMed=7675084;
Sands A.T., Abuin A., Sanchez A., Conti C.J., Bradley A.;

"High susceptibility to ultraviolet-induced carcinogenesis in mice
                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                               ö
                                                                                                                                                                                  XPC MOUSE STANDARD; PRT; 900 AA.
P51612; P54732;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
DNA-repair protein complementing XP-C cells homolog (Xeroderma pigmentosum group C complementing protein homolog) (P125).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L -> S (IN REF. 2).

RG -> TP (IN REF. 2).

EVQENM -> GVHEDT (IN REF. 2).

S -> N (IN REF. 2).

S -> N (IN REF. 2).

R -> S (IN REF. 2).
              DB 1; Length 824; 56;
                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA repair; DNA-binding; Muclear protein.

CONFLICT 28 30 AVN -> CSD (IN REF. 2)

CONFLICT 53 53 S -> L (IN REF. 2).

CONFLICT 70 70 L -> F (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:103557; Xpc.
GO; GO:0006289; P:nucleotide-excision repair; IMP.
InterPro; IPR004583; Rad4.
PF03835; Rad4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 KDA SUBUNIT (P58).
-1- SUBCELLULAR LOCATION: Nuclear (Probable).
-1- SIMILARITY: SOME, TO YEAST RAD4.
   93.8%; Scc. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPC gene.";
Nucleic Acids Res. 24:1026-1028(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIGRFAMS; TIGR00605; rad4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U27398; AAC52500.1; -. EMBL; U40005; AAA82720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 28-587 FROM N.A.
Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S70630; S70630.
MGD; MGI:103557; Xpc
                                                                                                        206 GFYRN 210
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FT CONFLICT 192 192 P -> L (IN REF. 2).

FT CONFLICT 342 345 GSRA -> ARP (IN REF. 2).

FT CONFLICT 428 428 R -> C (IN REF. 2).

FT CONFLICT 428 428 R -> C (IN REF. 2).

FT CONFLICT 584 428 R -> C (IN REF. 2).

FT CONFLICT 584 67 67 C -> S (IN REF. 2).

SQ SEQUENCE 900 AA; 100873 MW; 95737FCB36DC15DD CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 61;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 3 GFYRN 7

Db 182 GFYRN 186

Search completed: December 8, 2003, 09:14:13

Job time: 2.83838 secs
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December 8, 2003, 09:13:30 ; Search time 7.35354 Seconds (without alignments) 245.646 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                              830525 seqs, 258052604 residues
                                                                OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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%p_phage:*
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%p_rodent:*
%p_vrons:*
%p_vrrebrate:*
%p_vrrebrate:*
%p_vrrus:*
%p_rodenting:*
%p_bacteriap:*
%p_bacteriap:*
%p_archeap:*
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Gapop 10.0 ; Gapext 0.5
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sp_bacteria:*
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sp_invertebrate:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	08x3q1 escherichia	Osfiez escherichia	Q16938 ancylostoma	Q962v8 ancylostoma	Q9kyv8 streptomyce	P74345 synechocyst	Q8itp8 oesophagost	044490 anabaena va	Q9a2a6 caulobacter	O9taj9 cafeteria r	Ogvej2 drosophila	096723 drosophila	Q81803 triticum ae	O8tns2 methanosarc	OBdie9 synechococc	Q8yq65 anabaena sp
SUMMARIES	ID	Q8X3Q1	Q8FIE2	Q16938	Q962V8			QSITP8	Q44490		Q9TAJ9	Q9VGJ2	096723	Q8L803	Q8TNS2	Q8DIE9	QBYQ65
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228 2 Q8GMR5 230 12 Q8UXB5 237 17 Q9HPV4 264 16 Q8RTL4 264 16 Q8RTL4 325 17 Q8ZT12 325 19 Q8ZT12 361 16 Q8PA97 361 16 Q8PA97 361 16 Q8PB19 378 10 Q9CB49 475 10 Q9CB49 475 11 Q9DC65 475 3 Q9B58 475 11 Q9BC86 475 11 Q9BC86 475 11 Q9BC86 675 11 Q9BC86 676 10 Q8GRX1 533 11 Q91XK0 534 11 Q91XK0 534 11 Q91XK0 536 2 Q8G468 600 5 Q9NL27 611 10 Q8GZT8	ALIGNMER ALIGNMER rel. 20, Created) rel. 20, Last sequentel. 20, Last annots rel. 20, Last annots rel. 20, Last Bequentel. 20, Last annots rel. 20, Last Bequentel. 20, Last annots for II as annots Escherichia. Escherichia. Escherichia. Escherichia. Escherichia. Fac. III, Burland V. F. Eval. F. Eval.	100.0%; Pred. No. rative 0; Mismatch
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"Anticoagulant repertoire of the hookworm Ancylostoma caninum.";
EMBL, U30793; AAC47080.1; -. 93:2149-2154(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 03, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-coagulant protein C2 precursor (Fragment).
Ancylostoma caninum (Dog hookworm).
Eukaryota, Metazoa, Nematoda; Chromadorea, Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatinae; Ancylostoma.
NCBL TaxID=29170;
                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE=98298519; PubMed=9634780;
Jespers L.S., Messens J.H., De Keyser A., Eeckhout D.,
van den Brande I., Gansemans Y.G., Lauwereys M.J., Vlasuk G.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 9179 MW; 6709ABAOC8259BBB CRC64;
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016759; AAN79953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AA
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InterPro; IPR002919; TIL_Cysrich.
Pfam; PF01826; TIL; 1.
                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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Matches 5; Conservative
                                         PRELIMINARY;
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Q8FIE2;
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MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID=53326;
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                                                                                                         DB 5; Length 91; 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF399710; AAK81733.1; -. InterPro; IPR006209; EGF like. InterPro; IPR002919; TIL_Cysrich. Pfam; PF01826; TIL; 1. PROSITE; PS01186; EGF_2; 1.
                        ANTI-COAGULANT PROTEIN C2.
ECB11CB4597C24DA CRC64;
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20 102 ANTICOAGULANT PEPTIDE-1.
102 AA; 11834 MW; 315722980EF723E7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anticoagulant peptide-1 precursor.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC03187.
SC03187 OR SCE22.04.
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Pred. No.
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19 154 PUTATIVE TRYPSIN-LIKE INHIBITOR PROTEIN.
154 AA; 16564 MW; A7F566E3957DAB19 CRC64;
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MEDLINE=96016168; PubMed=7568132;
Thiel T., Lyons E.M., Erker J.C., Ernst A.;
"A second nitrogenase in vegetative cells of a heterocyst-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae; Caulobacter. TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBL_TaxID=1172;
                                                                                                                                                                       93.8%; Score 30; DB 5; Length 154; 100.0%; Pred. No. 87; 1. Indels tive 0; Mismatches 0; Indels
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89;
     "Identification of a male-specific nematode protein with
                         like inhibitor domains.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF399936; AAN32637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiel T., Lyons E.M., Erker J.C., Submitted (FRB-1996) to the EMBL/GenBank/DDBJ databases. EMBL, 149859; AAA93026.1; -
InterPro: IRRO4952; DUF269.
Ffam; PF03270; DUF269; 1.
SEQUENCE 158 AA, 17791 MW; D157EBF59C36FEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                     158 AA.
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SEQUENCE FROM N.A.
SEQUENCE 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
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01-JUN-2001 (TrEMBLrel. 17, La
01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical protein CC3660.
CC3660.
                                                                                                                                                   Query Match
Best Local Similarity luv.v.
S; Conservative
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                                                                                                                                    SEQUENCE
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SIGNAL
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Q9A2A6
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MBDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Kotani H., Tanaka A., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                   Gaps
                     Taylor K.,
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EMBL: D90914; BAA18439-1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 134 AA; 14545 MW; 7E5414E80FB43D10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oesophagostomum dentatum.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Strongyloidea; Chabertiidae; Oesophagostomum.
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939115; CAB971.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 110 AA; 10831 MW; 0893F0F52BBEA8FA CRC64;
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100.0%; Pred. No. 62;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein s1r1628.
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01-MAR-2003 (TrEMBLrel. 23, Last seg
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                       51 GPYRN 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=1148;
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                                                        Hopwood D.A.;
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P74345;
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Procone sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                        Score 30; DB 16; Length 172;
Pred. No. 97;
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"The mitochondrial genome of Cafeteria roenbergensis.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF193903; AAF05787.1; --
                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 172 Aa; 18425 MW; 5DD52E712F406F6A CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity 100.0
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NCBI_TaxID=7227;
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I-T OR CG14719.
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RP SEQUE
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon G.G., Wortman J.R., Tandell M.D., Zhang O., Chen L.X.,

Brandon G.G., Mortman J.R., Mandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,

R. Abril J.F., Aspbayari A., An H.-J., Andrews-Pfannkoch C., Bealey E.M.,

Ballew R.M., Besu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

Berkova D., Botchan M.R., Buuck J., Brokstein P., Brottler P.,

Burtis K.C., Busam D.A., Butler H., Caddau B., Center A., Chandra I.,

R. Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottler P.,

Burtis K.C., Eusam D.A., Butler H., Caddau B., Center A., Chandra I.,

R. Double B., Delcher A., Deng Z., Mays A.D., Dew I., Diates P.,

Burbin K.J., Evangalista C.C., Ferraz C., Ferriera S., Pleischman W.,

R. Poblos B., Delcher A., Deng Z., Mays A.D., Dew I., Diates P.,

B. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

R. Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,

R. Alashi M., Kalush F., Karpen G.H., Ke Z., Gubar P., Harris M.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Gubar P., Houck J.,

R. Kimmel B.E., Kodirac C.D., Kraft C., Kratiz S., Mosherson D.L.,

R. Markino G.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

R. Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

R. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier E., Spradlind A.C., Stapleton M., Stupski M.P., Sanith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Sanith T.,

Shen S., Wan R., Woodage T., Worley K.C., Wu D., Yang S., Yao,

R. Wang S.H., Rhong F.N., Rhong W., Weissenbach J.,

R. Wenger E., Sharl-Kamos I., Shapson M., Stupski M., Wood S., Zhan M., Weissenbach J.,

R. Wenger E., Shadler-Kamos I., Shapson M., Stupski M., Wood S., Zhan M., Venter J.C.;

R. Wenger E., Shadler-Kamos I., Shapson W., Sun S.,

R. Wenger F. Phongon F.N., Rhong W., Venter J.C.;

R. Wenger F. Phongon F.N., Rhong W
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Helps N.R., Vergidou C., Gaskell T., Cohen P.T.W.;
"Characterisation of a novel Drosophila melanogaster testis specific
PPI inhibitor related to mammalian inhibitor-2: identification of the
site of interaction with PPI.";
FEBS Lett. 438:131-136(1998).
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Boptera, Endopterygota, Diptera; Brachycera; Muscomorpha;
Bohydroidea, Drosophilidae, Drosophila.
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Query Match
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QBDIE9
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STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
MEDLINE=21929760; PubMed=11932238;
MEDLINE=21929760; PubMed=11932238;
MEDLINE=21929760; PubMed=11932238;
FitzHugh W., Calvo S., Bngels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
                                                                                                                                                                                         Gaps
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OMAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative plastid ribosomal protein CL9.
Triticum aestivum (Wheat).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
NCBI_TaxID=4565,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu Z.-X., Laroche A., Gaudet D.;
"Triticum aestivum putative plastid ribosomal protein CL9 gene.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY123421; AAM92711.1;
InterPro; IPR000244; Ribosomal L9.
Pfam; PF03948; Ribosomal L9-C; 1.
Pfam; PF01281; Ribosomal L9-C; 1.
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                                                                                                                                     93.8%; Score 30; DB 5; Length 184; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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                                             21 A -> T.
183 D -> G.
20988 MW; D697139E7271A7B2 CRC64;
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TRKA OR MA2210.
Methanosarcina acetivorans.
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PROSITE; PS00651; RIBOSOMAL L9; 1.
EMBL; AJ006867; CAA07278.1; -. FlyBase; FBgn0025821; I.t. VARIANT 21 21 A
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                                                                                                                                                          Best Local Similarity 100.(
Matches 5; Conservative
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                                                                                          184 AA;
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SEQUENCE 191 AA;
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Q8L803
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RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C., RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., RA Fritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander B., RA Metcalf W.W., Birren B.;

RA Moscolia diversity ";

Genome Res. 12:532-542(2002).

BR EMBL, ARO10907; ARM05606.1;

BR EMBL, ARO10907; ARM05606.1;

BR EMBL, ARO10907; ARM05606.1;

RA Complete proteome.

SR SRUGENCE 216 AA.
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MEDLINE=2225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamotc Watanabe A., Iriguchi M., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 30; DB 17; Length 216; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Endonuclease III.
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EMBL; APOUSJ74; BAC09193.1; -
Complete proteome.
SEQUENCE 222 AA; 25106 MW;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 8, 2003, 09:13:30; Search time 2.89899 Seconds (without alignments) 232.212 Million cell updates/sec Run on:

US-09-498-556C-79 32 1 XXGFYRN 7

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
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	21020	יימרכוו	Transcri	9 !	ar .	Description
-	30	93.8	77	~	9	unknown protein en
7		93.8	134	7	S76180	hypothetical prote
e	30	93.8	172	7	B87703	conserved hypothet
4		93.8	175	~	S73496	hypoxanthine-quani
Ŋ	30	93.8	175	7	F64250	hypoxanthine-quani
9	30	93.8	223	7	AC2302	endonuclease III [
7	30	93.8	226	~	C70790	probable Endonucle
80	30	93.8	237	~	G84299	hypothetical prote
σ	30	93.8	361	~	AG0169	phosphoserine tran
10	30	93.8	362	7	C82572	phosphoserine amin
11	30	93.8	408	~	T25524	hypothetical prote
12	30	93.8	415	N	T46716	hypothetical prote
13	30	93.8	465	7	A96553	
14	30	93.8	481	~	850053	tryptophan-tRNA li
15	30	93.8	533	Н	YRMSCS	monophenol monooxy
16	30	93.8	747	~	T16274	hypothetical prote
17	30	93.8	824	7	S40937	
18	30	93.8	900	~	S70630	D.
19	30	93.8	940	~	S44345	xeroderma pigmento
20	30	93.8	1041	~	C87645	AcrB/AcrD/AcrF fam
21	30	93.8	1564	~	855517	probable transport
22	27	84.4	36	7	H70251	hypothetical prote
23	27	84.4	9	Н	F70187	ribosomal protein
24	27	84.4	199	~	T39498	hypothetical prote
	27	84.4	201	0	A86636	
56	27	84.4	234	~	A84993	0
27	27	84.4	258	~	T22092	hypothetical prote
28	27	84.4	275	7	A69413	conserved hypothet
53	27	84.4	299	~	F64491	hypothetical prote

aad 5'-region hypo	hypothetical prote	hypothetical prote	endonuclease III -	acetyl-CoA synthet	uncharacterized co	v-type sodium ATP	unknown protein en	hypothetical prote	ycjx protein - Esc	probable enzyme (i	probable EC 2.1 en	probable ATP-bindi	tryptophan-tRNA li	peptidyl-prolyl ci
B36972	D69414	C75004	E64376	F69193	F96994	E95152	H85745	C90873	D64881	D90866	E85752	AC0659	A41706	862590
318 2	340 2	340 2	353 2	425 2	426 2	461 2	463 2	463 2	465 2	465 2	465 2	465 2	471 1	471 1
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protein encoded by prophage CP-933C [imported] - Escherichia coli (strain 0157:1

C;Species: Escherichia coli (Briain Ols):ii
C;Species: Escherichia coli (Briain Ols):ii
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17. Forbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli Ol57:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85684
A;Accession: B85684
A;Accession: preliminary
A;Accession: preliminary
A;Accession: Jr7 csTo>
A;Accession: B85684
A;A

.. 0 Length 77; 0; Indels Query Match 93.8%; Score 30; DB 2; Best Local Similarity 100.0%; Pred. No. 9.8; Matches 5; Conservative 0; Mismatches

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Gaps

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876180

hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76180
C;

A; Reference number: S74322; MUID:97061201; PMID:8905231

A; Accession: S76180

A.Status: preliminary A.Molecule type: DNA A.Residues: 1-134 <KAN> A.Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18439.1; PID:d10191' A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Gaps .. 0 Query Match 93.8%; Score 30; DB 2; Length 134; Best Local Similarity 100.0%; Pred. No. 17; Matches 5; Conservative 0; Mismatches 0; Indels

GFYRN 31

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7 GFYRN

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Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; Fluhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.R.C.A.; Venter, J.C.
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A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Attele: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A.Reference number: A70500; MUID:98295987; PMID:9614230

A.Accession: C70790

A.Accession: C70790

A.Accession: C70790

A.Accession: CANDON, MUID:98295987; PMID:9614230
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A;Experimental source: strain G-37
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G;Species: Nostoc sp. grain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC3102
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Molecule type: DNA
A;Residues: 1-223 «KUR»
A;Residues: 1-223 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB75669.1; PID:g17133104; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                               . C.A.; Venter, J.C. Science 270, 397-403, 1995
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Nelecule type: DNA
A;Residues: 1-175 <TIGR>
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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29;
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C;Superfamily: apurinic/apyrimidinic endonuclease III
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C;Superfamily: hypoxanthine phosphoribosyltransferase
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73 GFYRN 77

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3 GFYRN 7

Matches

A;Gene: CC3660

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A, Residues: 1-226 <COL>
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conserved hypothetical protein CC3660 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: B87703
B; i.aub, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; i.aub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87703
A;Accession: B87703
A;Molecule type: DNA
A;Residues: Jr2 cSTO>
C;Genetics: Caulobacter C
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22;
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100.0%; Pred. No. ....
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Matches 5; Conservative
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Best Local Similarity
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3 GFYRN 7

Query Match

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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: C82572
C;Accession: C82572
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Cross-references: GB:AE004043; GB:AE003849; NID:g9107486; PIDN:AAF85125.1; GSPDB:GN001
A;Cross-references: GB:AE004043; GB:AE003849; NID:g9107486; PIDN:AAF85125.1; GSPDB:GN001
B;Cross-references: GB:AE004043; GB:AE003849; NID:g9107486; PIDN:AAF85125.1; GSPDB:GN001
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, I
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
Bsubmitted to GenBank, June 2000
A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
J.D.; Junqueira, M.L.; Madelra, A.M.B.N.; Madrio, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menock, C.L.; Marques, W.V.; Matthors: Martins, E.M.F.; Matsukuma, A.Y.; Menock, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
                                                                                                                                                                                                                                                                                                     phosphoserine aminotransferase XF2326 [imported] - Xylella fastidiosa (strain 9a5c)
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A;Molecule type: DNA
A;Residues: 1-408 <-DAVA
A;Residues: 1-408 <-DAVA
A;Cross-references: EMBL:U97193; PIDN:AABS2442.1; GSPDB:GN00019; CESP:C06A5.9
A;Experimental source: strain Bristol N2; clone C06A5
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Introns: 3/1; 27/3; 86/1; 154/1; 201/3; 240/3; 268/3; 297/3
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R;Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C06A5.
A;Reference number: Z20044
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rive 0; Mismatches
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Pred. No.
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Best Local Similarity 100.0
Matches 5; Conservative
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Matches 5; Conservative
                                                                                       283 GFYRN 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: annotation
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             3 GFYRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng1457c [imported] - Halobacterium sp. NRC-1
C'Species: Halobacterium sp. NRC-1
C'Species: Na-Deb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C'Accession: G84239
RiNg, W.V.; Kennedy, S.F.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA17996.1; PID:g296009
A;Experimental source: strain H37Rv
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0169
C;Accession: Accession: Acces
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                                                                                                                 A,Gene: nth
C,Superfamily: apurinic/apyrimidinic endonuclease III
C,Superfamily: aton-sulfur protein; metalloprotein
C,Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein
E;179,186,189,195/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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A;Gene: VNG1457C
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A;Cross-references: GB:AL590842; PIDN:CAC90218.1; PID:g15979438; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Best Local Similarity 100.0
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C;Superfamily: phosphoserine
C;Keywords: aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-237 <STO>
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A; Status: preliminary
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A; Status: preliminary
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monophenol monooxygenase (EC 1.14.18.1) precursor (validated) - mouse monophenol monophenol oxidase; phenolase; tyrosinase C;Species: Mus musculus (house mouse)
C;Species: Mus-1989 #sequence revision 11-Mar-1989 #text_change 20-Apr-2000
C;Accession: A27711; A60778; A32429; B33429; B301170; S02278; S15753; I49736
R;Kwon, B.S.; Wakulchik, M.; Haq, A.K.; Halaban, R.; Kestler, D.
Biochem: Biophys. Res. Commun. 153, 1301-1309, 1988
A;Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its A;Reference number: A27711; MUID:88268910; PMID:3134020
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R;Kwon, B.S.; Haq, A.K.; Wakulchik, M.; Kestler, D.; Barton, D.E.; Francke, U.; Lamoreux,
J. Invest. Dermatol. 93, 589-594, 1989
                                                                                                                                A;Title: An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthemagner number: $50052; MUID:9501826; PMID:7932716
A;Accession: $50053
A;Cross-references: EMBL:X69657; NID:955437; PIDN:CAA49348.1; PID:955438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology C;Superfamily: mammalian tryptophan-tRNA synthetase; ligase; protein biosynthesi: F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicted F;1-487/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>
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C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002 C;Accession: S50053; S50052; I49391; S31461; S31462 C;Recision: S50053; S50052; I49391; S31461; S31462 B; Sarger. C.; Bonnet, J.; Garret, M. J. Mol. Biol. 242, S99-603, 1994
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A;Residues: 1-533 <KWO>
A;Cross-references: GB:M20234; NID:g202247; PIDN:AAA40516.1; PID:g202248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y, Cross-references: EMBL: X69656; NID: 955435; PIDN: CAA49347.1; PID: 955436; Genetics: SSF; Kisselev, L.L.; Midchimie 75, 1027-1039, 1993; Arther Mammalian tryptophanyl-tRNA synthetases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: EMBL:X69657; NID:955437; PIDN:CAA49348.1; PID:955438
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A;Note: intron position was determined by sequencing of genomic DNA
A;Accession: S50052
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62;
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A;Note: the list of introns may be incomplete; clone W13
C;Genetics: <SSF>
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A,Molecule type: DNA
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A;Molecule type: DNA
Residues: 1-273 <KR2>
A;Experimental source: BALB/c
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Matches
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C'Species: O2-Mar-2001
C'Accession: A96553
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Anutre 408, 816-820, 2000
A,Authors: Hunder, J.L.; Jankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A96553
A;Status: preliminary
A;Accession: As6553
A;Cross-references: GB:AE005173; NID:g10092358; PIDN:AAG12767.1; GSPDB:GN00141
A;Gene: F5D21.17
A;Map position: 1
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                               C; Species: Leishmania major
C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C; Accession: T46710
C; Accession: T46710
Bubmitted to the EMBL Data Library, December 1999
A; Reference number: Z23137
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 30; DB 2; Length 465; 100.0%; Pred. No. 60; 1. Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               protein L4326.05 [imported] - Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tryptophan-tRNA ligase (EC 6.1.1.2) alpha-2 chain - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL121861; PIDN:CAB58381.1 A;Experimental source: strain Friedlin C;Genetics: A;Note: L4326.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                           229 GFYRN 233
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Gaps

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A; Status: translation not shown
A; Status: translation not shown
A; Status: translation not shown
A; Residues: 1-13 < SHI>
A; Cross-references: EMBL:XS1743; NID:955057; PIDN:CAA36033.1; PID:955058
A; Experimental source: strain BALB/C
R; Kwon, B.S.; Halaban, R.; Chintamanen; C.
Biochem. Biophys. Res. Commun. 161, 252-260, 1989
A; Title: Molecular basis of mouse Himalayan mutation.
A; Reference number: 149736; MUD:89273644; PMID:2567165
A; Accession: 149736
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Minlecule type: mRNA
A; Residues: 1-39, I', 41-102, 'C', 104-196,'Q', 198-345,'G', 347-419,'R', 421-533 < RES>
A; Cross-references: GB:M26729; NID:9193845; PIDN:AA37806.1; PID:9309296
C; Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it reactions in the formation of pigments such as melanins and other polyphenolic compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: Tyri
A;Gene: Tyri
A;Gene: Tyri
A;Gene: Tyri
A;Gene: Tyri
A;Gene: Tyri
C;Superfamily: monophenol monooxygenase
C;Keywords: albinism; alternative splicing; copper; glycoprotein; melanin biosynthesis;
C;Keywords: albinism; asquence #status predicted <SIG>
C;Keywords: albinism; sequence #status predicted <SIG>
F;19-53/Product: monophenol monooxygenase #status predicted <AMT>
F;474-497/Domain: transmembrane #status predicted <AMN>
F;86,111,161,230,337,371/Binding site: carbohydrate (Asn) (covalent) #status predicted
and A** Score 30; DB 1; Length 533;
A** Gabs 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X12782
A;Note: part of this sequence was confirmed by protein sequencing
R;Shibahara, S.; Okinaga, S.; Tomita, Y.; Takeda, A.; Yamamoto, H.; Sato, M.; Takeuchi,
Eur. J. Blochem. 189, 455-461, 1990
A;Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cyst
A;Reference number: S15753; MUID:90249393; PMID:2110899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Nolecule type: mRNA
A;Residues: 1-102,'C',104-263,'I',265-345,'G',347-533 <MUE>
A;Crose-references: G8:X12782,'NID:g55061; PIDN:CAA31273.1; PID:g55062
R;Yamamocto, H.; Takeuchi, S.; Kudo, T.; Makino, K.; Nakata, A.; Shinoda, T.; Takeuchi,
Jpn. J. Genet. 62, 271-274, 1987
A;Title: Cloning and sequencing of mouse tyrosinase cDNA.
                                      iochem. Biophys. Res. Commun. 159, 848-853, 1989
Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.
Reference number: A32429; MUID:89193679; PMID:2494997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Experimental gource: Bi6 melanoma cells
R/Mueller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.
BMBO J. 7, 2723-2730, 1988
A/Fitle: Functional analysis of alternatively spliced tyrosinase gene transcripts.
A/Reference number: S01170; MUID:89030636; PMID:3141148
                                                                                                                                                              A;Accession: A32429
A;Molecule type: mRNA
A;Residues: 1-102, C', 104-345, 'G',347-533 <TER>
A;Cross-references: GB:M24560; NID:g202249; PIDN:AAA40517.1; PID:g202250
R; Terao, M.; Tabe, L.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-102,'C',104-263,'I',265-345,'G',347-448 <YAM>
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A;Residues: 1-77;155-345,'G',347-533 <TE2>
A;Cross-references: GB:M24560
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Job time: 4.89899 secs
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A;Accession: S02278
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                                                                                                                                                                                                                                                                                                                                Accession: B32429
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 0.0%
Matches 0; Conservative
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TYPE: AMINO ACID
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TOPOLOGY:
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                                                                    December 8, 2003, 09:13:31 ; Search time 1.85859 Seconds (without alignments) 91.060 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-791-213D-40
US-08-174-365A-57
US-07-789-913-23
US-08-049-794-23
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US-08-675-354-25
US-08-675-318-25
US-08-965-918-25
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S-07-791-213D-24
S-07-791-213D-40
S-08-174-365A-57
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US-08-613-400A-23
US-08-613-400A-25
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                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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31, Appl
31, Appl
45, Appl
22, Appl
112, Appl
22, Appl
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16, Appl
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10, Appl
11, Appl
11, Appl
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ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
TITING DATE: 19920113
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Sequence 12, Application US/07820154A

Patent No. 3882425

GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
US-08-801-092-10
US-08-801-092-17
US-08-801-092-24
US-08-801-092-31
US-08-801-092-38
US-09-298-017-23
US-09-298-017-23
US-09-298-017-25
US-09-392-979A-23
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0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12:
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TELEFAX: (212)664-0525
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Sequence 57, Application US/08174365A

Patent No. 5478809

GENERAL INFORMATION:
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: MAXTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-791-213D-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                     GENERAL INPORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: MORISHITA, Hideaki
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, MSABAID:
TITLE OF INVENTION: SANE BAD ENCORSS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: TREATING USING THE SAME
TITLE OF INVENTION: TREATING USING THE SAME
ANDRESSES:
ANDRESSESS:
ANDRESSES:
ANDRESSESSES:
ANDRESSESSES:
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ANDRESSESSES
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Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: PAMPARA, MASAHIRO
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: BULDS, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%; Pred. No. 0;
tive 0; Mismatches
Sequence 24, Application US/07791213D Patent No. 5409895
GENERAL INFORMATION:
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STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.0
Best Local Similarity 0.0%
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide US-07-791-213D-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 X 1
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Gaps ö

1; Indels

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Score 0; DB 1; Length 1; red. No. 0;
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: Floppy disk
COMPUTER: F
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MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/174,365A
FILING DATE: December 28, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```
Sequence 25, Application US/07789913

Patent NO. 5559095

GENERAL INFORMATION:
APPLICANT: Miljainch, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Pox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Biner, Robert S.
                                ; INDIVIDUAL ISOLATE: peptide fragment used in the claims US-07-789-913-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
CRIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-25
                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                 Length 1;
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ZIP: 94306

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
TITING DATE: 1911112
                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                              Score 0; DB 1;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPRANE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.0%; Score 0; DB 1
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
                                                                                                                                 0.0%;
                                                                                                                           Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1 amino acids TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  both
      ORIGINAL SOURCE
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US-07-789-913-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                               Sequence 23, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Pox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Walentino, Karen L.
APPLICANT: Walentino, Donald H.
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTOMEV/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    0.0%; Score 0; DB 1;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 365-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                     NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Conservative
SEQUENCE CHARACTERISTICS
                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: Law Office STREET: 350 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
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US-07-789-913-23
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Gaps

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Sequence 12, Application US/08433037
Patent No. 5707828
GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikanyadan
APPLICANT: Barr, Kathryn A.
APPLICANT: Tachop, Juerg F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
CORRESPONDENCES: 19
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BHYANCING OPIATE ANALGESIA INTILE OF INVENTION: BHYANCING OPIATE ANALGESIA NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESSE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
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                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFROME: (415) 324-0960

INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 0.0%
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-049-794-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
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                                                                                                                                                                                                                 Sequence 23, Application US/08049794

Patent No. 5587454

GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WINDENTINO, KAREN L
APPLICANT: WINDENTINO, RAFFOR C
APPLICANT: WILDIANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAW OFFICES OF PETET Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
| INDIVIDUAL ISOLATE: 32 US-08-049-794-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 1930415

CLASSIFICATION NUMBER: US/08/049,794

FILING DATE: 1930415

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: S865-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEBRONE: (415) 324-0860

INFORMATION FOR SEQ ID NO: 23:

SEQUIENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto CONTREE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08049794
Patent No. 5587454
SENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
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US-08-049-794-25
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0; Gaps

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RESULT 11
US-07-869-933-16
Sequence 16, Application US/07869933
Sequence 16, Application US/07869933
Fatent No. 5770396
TITLE OF INVENTION:
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: IMMUNOGLOBULIN
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
SCORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ZIP: 22313-0299
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDERS: US/07/869,933
FILING DATE: 19920016
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                 Score 0; DB 1;
Pred. No. 0;
0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFRAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 0;
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US-08-293-150A-24
; Sequence 24, Application US/08293150A
                                                                                                                                                                                                                                                                                                                                                              Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
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                                                          TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-606-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 amino acids
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                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-869-933-16
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 9108Z
TELEFORMUNICATION INFORMATION:
TELEFORM (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Matalssan
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION NDATA:
APPLICATION NDAER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION NUMBER: ES 9203753-0
FILING DATE: 11-DEC-1992
ATPONEY/AGENT INFORMATION:
AMADE: ADMINIST PROFAMILION:
AMADE: ADMINIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0; 0; 0; 0; 0; 0; 0; Mismatches
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ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
STRATE: D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Amernick, Burton A.
REGISTATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08448606
Patent No. 5721114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Abraha
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Virginia
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US-08-293-150A-40
i Sequence 40. Application US/08293150A
j Patent No. 5792629
j GENERAL INFORMATION:
APPLICANT: MONISHITA, Hideaki
APPLICANT: KANAMORI, TOSHINOTI
APPLICANT: KANAMORI, TOSHINOTI
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                  APPLICANT: KANAMORI, TOSHINOTI
APPLICANT: NOBUHARA, MSEAHICO
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 1404
CITY: Alexandria
STREET: VIEGINIA
COUNTRY: United States
ZIP: 22313-1404
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-LUCS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
ATFORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
TELEFRAM: (703) 836-6620
SEQUENCE CHARACTERISTICS:
LUNGTH: LAMINO acids
LUNGTH: LAMINO acids
LUNGTH: LAMINO acids
LUNGTH: LAMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 0.0%;
Matches 0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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US-08-496-847-23
; Sequence 23, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
APPLICANT: Bowersox, Stephen S. APPLICANT: Gohil, Kishorchandra
APPLICANT: Adviacensens, Peter I. APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: PCRMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                      OPERATING SYSTEM: PC-LUOS/MS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELEFONM: (703) 836-620
TELEFONM: (703) 836-620
TELEFONE: (703) 836-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIPICATION: 514
ATTOCNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 0; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
ZIP: 22313-1404
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.0%;
Best Local Similarity 0.0%; Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 amino acids
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Gaps

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1; Indels

Pred. No. 0; 0; Mismatches

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Search completed: December 8, 2003, 09:20:29 Job time : 1.85859 secs
  Best Local Similarity 0.0%;
Matches 0; Conservative
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APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                         Length 1;
                                                                                                                                                                 TYPE: amino acid
TOPOLGA: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONOPEPTIDE GROUP 1 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: US
ZIP: 94306-1546
COMPUTER: READDALE FORM:
MEDUTUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRSESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-UNN-1995
CLASSIFICATION: 514
ATTORNEY/AGBNT INFORMATION:
NAME: STRATFORM INFORMATION:
NAME: STRATFORM NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
TELEPHONE: 650-324-0880
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTER/STICS:
LENGTH: 1 amino acids
                                                                                                                                                                                                                                                                                                                                     Score 0; DB 1;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                        5865-0009.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08496847
Patent No. 5795864
REGISTRATION NUMBER: 34,444
                     REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 0.0%; 1
Matches 0; Conservative
                                                                              TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
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INDIVIDUAL ISOLATE:
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TOPOLOGY: linear
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0.0%; Score 0; DB 1; Length 1;

Query Match

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Sequence Sequence Sequence

Sequence

Sequence Sequence

Sequence

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Sequence

OM protein

Run on:

Sequence:

Searched:

Database

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Sequence 4, Application US/09909348

Fatent No. US2002004237341

GENERAL INFORMATION:

APPLICANT: Carney, Darrell H.

APPLICANT: Crowther, Roger S.

APPLICANT: Crowther, John

TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists

TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin R.

FILE REFERENCE: 3033.1003-001

CURRENT PILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 60/219,800

PRIOR APPLICATION NUMBER: US 60/219,800

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 4

FERDITATION NO 4.
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OTHER INFORMATION: Xaa at position six is Glu or Gln
OTHER INFORMATION: Xaa at position thirteen is Phe, Met,
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US-09-982-172-93
US-09-982-172-105
US-09-982-172-106
US-09-982-172-120
US-09-982-172-120
US-09-982-172-124
US-09-982-172-149
US-09-982-172-149
US-09-982-172-149
US-09-982-172-172
US-09-982-172-173
US-09-982-172-173
US-09-982-172-173
US-09-982-172-173
US-09-982-172-195
US-10-013-221B-195
US-10-013-221B-195
US-10-013-221B-195
US-10-061-607A-28
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Pred. No. 0;
0; Mismatches
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ORGANISM: Artificial Sequence
     Query Match
Best Local Similarity 0.0%
Matches 0; Conservative
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US-09-909-348-4
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Sequence 1
Sequence 3
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'(gnz_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
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'(gnz_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
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                          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-982-172-4
US-09-982-172-19
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US-09-982-172-31
US-09-982-172-35
US-09-982-172-46
US-09-982-172-60
US-09-982-172-60
US-09-982-172-81
US-09-982-172-81
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US-09-982-172-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                         TYPE: PRT
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     Sequence 3, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Islael Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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Sequence 4, Application US/09982172

Bacent No. US20020137119A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: UTILIZING EACH
FILE OF INVENTION: UTILIZING EACH
FILE REPRENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1

SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-3
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence
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US-09-982-172-3
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GENERAL INFORMATION:

APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT)
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UNMER: US/09/982,172
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19
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Pred. No. 0;
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SEQ ID NO 9
LENGTH: 1
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US-09-982-172-11
Sequence 11, Application US/09982172
; Patent No. US2002013711941
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Patent No. US20020137119A1
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ORGANISM: Artificial sequence
                                                                                                                                                                            ORGANISM: Artificial sequence
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Best Local Similarity 0.0%;
Matches 0; Conservative
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Best Local Similarity
Matches 0; Conserv
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Sequence 37, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT PILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin Version 3.1

FEMALE: 10 37
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APPLICANT: Enil 1 staci Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI:

TITLE OF INVENTION: UTILIZING EACH

FITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22233

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT APPLICATION NUMBER: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1
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APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTILIZING EACH
FILE REPRENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
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; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-37
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Pred. No. 0;
0; Mismatches
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Pred. No. 0;
0; Mismatches
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 0; Conservat
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Patent No. US20020137119A1

Patent No. US20020137119A1

APPLICANT: Entl Israel Katz

TITLE OF INVENTION: DEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT PILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                        APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTLIZING EACH
FILE REPERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 31
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Pred. No. 0;
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                Score 0; DB 1
Pred. No. 0;
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         Query Match 0.0
Best Local Similarity 0.0%
Matches 0; Conservative
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Best Local Similarity 0.0*
Matches 0; Conservative
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GENERAL INFORMATION:
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Sequence 83, Application US/09982172

Sequence 83, Application US/09982172

BREENT NO. USZOGOJ37119A1

GENERAL INFORMATION:
APPLICANT: Enil larael Katz

ITILE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTERFECT AND ANTIBODIE.

ITILE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATION TITLE OF INVENTION: UTILIZED BEACH

ITILE REPERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 83

LENGTH: 1
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US-09-982-172-86

is Sequence 86, Application US/09982172

sequence 86, Application US/09982172

sequence 86, Application US/09982172

general No. US20020137119A1

general No. US20020137119A1

general INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ULLIAING BACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin Version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 0.0%;
Matches 0; Conservative
Best Local Similarity 0.0%;
Matches 0; Conservative
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US-09-982-172-83
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Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION:
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REPERENCE: 0/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80. Application US/09982172

Factor No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT PILING DATE: 2001-10-19

SOFTWARE: Patentin version 3.1

SEQUENCE OF METHOD WAS 1.1

SEQUENCE OF METHOD WAS 1.1
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0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                       DB 10; Length 1; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-80
                                                                                                                                                                 OTHER INFORMATION: Computer generated synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                     Query Match 0.0%; Score 0; DB 1
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0%; Score 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
                                                                                               TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                  1 X 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-982-172-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-982-172-81
                                                                                                                                                                                           US-09-982-172-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                FEATURE:
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GenCore version 5.1.6
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2003, 09:13:30 ; Search time 34.7879 Seconds	(without alignments)	232.212 Million cell updates/sec
8,		
December		
Run on:		

Title: US-09-498-556C-59 Perfect score: 486 Samience: 1 Kammordenbryneckser

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKIES	
Result	9	Query		5	f	
	Score	Macch	rengen	3	TD	Description
п	125	25.7	561	~	T27318	hypothetical prote
7	125	25.7	626	~	T27319	
m	113	23.3	490	~	T32003	_
4	112	23.0	249	~	T24604	
Ŋ	109.5	22.5	1642	~	T19130	_
9	105.5	21.7	145	~	T15608	
7	100	20.6	5376	~	T42215	
80	66	20.4	1036	~	T17405	scavenger receptor
60	98.5	20.3	135	~	T15610	hypothetical prote
10	96	20.2	137	~	T15609	
11	96.5	19.9	869	Н	JC4858	ы
12	95.5	19.7	166	~	H89044	•
13	94.5	19.4		~	C89046	protein C10G8.4 [i
14	94.5	19.4	4660	~	T42737	gp330 protein prec
15	92.5	19.0	63	~	S07127	chymotrypsin/elast
16	92.5	19.0	63	~	S08572	chymotrypsin/elast
17	92.5	19.0	4753	Н	A47437	LDL-receptor-relat
18	90.5	18.6	195	7	T28803	hypothetical prote
19	87.5	18.0	802	~	T24293	
20	87.5	18.0	949	~	T24294	
. 21	85.5	17.6	863	Ч	S51789	VLDL receptor prec
22	B	17.5	2155	0	T30197	alpha tectorin - m
23	84.5	17.4	13288	~	T03099	mucin, submaxillar
24	83	17.1	209	7	T02394	hypothetical prote
25	٠	17.0	873	-	A49729	VLDL receptor prec
56	82.5	17.0	873	Н	QRRBVD	VLDL receptor prec
27	82	16.9	62	~	835098	trypsin inhibitor
28	œ	16.9	267	7	T30007	hypothetical prote
29	81.5	16.8	1810	-	A32230	υ

tenascin-X - bovin	hypothetical prote	probable tenascin	von Willebrand fac	fibrillin 1 precur	hypothetical prote	tenascin - eastern	integrin beta-1 ch	protein unc-52 [im	mucin MUC5B, trach	protein unc-52 [im	hypothetical prote	B cell-associated	hypothetical prote	probable vitelloge	hemocytin - silkwo
T42629	T15611	T09070	VWHU	A47221	T16642	A43902	A28193	F88369	JE0352	C88369	T19821	A46476	T15884	T18308	852093
7	~	~	-	~	N	7	~	7	~	7	~	~	N	~	0
4135	169	4006	2813	3002	548	647	798	1160	1321	2295	3375	305	1107	1847	3133
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16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
81.5	80.5	80.5	79.5	79.5	79	79	78.5	78.5	78.5	78.5	78.5	78	78	78	78
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-561 <WIL>
A;Cross-references: EMBL:Z98877; PIDN:CAB54472.1; GSPDB:GN00023; CESP:Y69H2.3a
A;Experimental source: clone Y69H2
C;Genetics:
A;Gene: CESP:Y69H2.3a
                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27318
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 25.7%; Score 125; DB 2; Length 561; Best Local Similarity 36.1%; Pred. No. 0.00025; Matches 26; Conservative 10; Mismatches 16; Indels 20;
                            hypothetical protein Y69H2.3a - Caenorhabditis elegans
                                                                                                                                                                                          submitted to the EMBL Data Library, August 1997 A;Reference number: Z20343 A;Accession: T27318
127318
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5 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQ-----DCVCEEGFYRN 59

Gaps

60 KDDKCVSAEDCE 71 ð 셤 ઠ

RESULT 2

543 NSGKCVTQNDCD 554

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hypothetical protein Y69H2.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tarilis elegans
C;Accession: T27319
R;McMurray, A.
Submitted to the EMBL Data Library, August 1997
A;Reference number: 220343
A;Accession: T27319
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Rēsidues: 1-626 <WIL> A;Cross-references: EMBL:Z98877; PIDN:CAB54473.1; GSPDB:GN00023; CESP:Y69H2.3b A;Experimental source: clone Y69H2

A; Gene: CESP: Y69H2.3b C;Genetics:

A;Map position: 5 A;Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3

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66 VRRLEC 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
                                                                                                                                                                                                                                                                                                                                          RESULT 5
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-490 < dDNA>
A,Cross-references: EMBL:AF016668; PIDN:AAB66095.1; GSPDB:GN00020; CESP:F36H9.4
A,Experimental source: strain Bristol N2; clone F36H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 17-Mar-2000
C;Accession: T24604
R;Mortimore, B.
R;M
                                                                                                                                                                                                                  2 ATMOCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV-----PCLVRVCHQDCVCEEGF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 APKKCGPNEDFKECGT-ACEANC-----AEGHVMFCTMQCIVNVCQ----CKDGF 64
                                                                                                                                                                       5 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQ-----DCVCEEGFYRN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F36H9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32003 #squence_revision 29-Oct-1999 #text_change 29-Oct-1999 R;Dante, M.; Kramer, U.; Twyman, B. aubmitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid F36H9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 2
A;Introns: 5/3; 22/1; 46/3; 72/3; 199/2; 220/3; 278/3; 306/2; 345/3; 427/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                          Gaps
Query Match 25.7%; Score 125; DB 2; Length 626; Best Local Similarity 36.1%; Pred. No. 0.00027; Matches 26; Conservative 10; Mismatches 16; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.3%; Score 113; DB 2; Length 490; Best Local Similarity 34.7%; Pred. No. 0.0029; Matches 25; Conservative 9; Mismatches 18; Indels 20;
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A;Map position: 3
A;Introns: 17/1; 54/1; 78/2; 140/1; 164/2; 207/3
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.09
Best Local Similarity 34.89
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        608 NSGKCVTQNDCD 619
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                                                                                                                                                                                                                                                                                                                                          60 KDDKCVSAEDCE 71
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain Bristol N2
A;Experimental source: strain Bristol N2
A;Gene: CESP:C35E10.7
A;Introns: 39/3
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                                 185 CGPNEHFVGCKNICSDTKC-----NEKRKMCPAVCTFPGCVCLNGFFRDKHDKCV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rismye, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19078
A;Accession: T19130
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1642 - WIL>
A;Cross-references: EMBL:Z81465; PIDN:CAB03861.1; GSPDB:GN00020; CESP:C09F9.2
A;Experimental source: clone C09F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15608
                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C09F9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QCGENEKYDSC--GSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYR--NK
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6 CGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNKDDKCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.5%; Score 109.5; DB 2; Length Best Local Similarity 33.8%; Pred. No. 0.016; Matches 24; Conservative 11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2
A;Introns: 75/3; 103/2; 220/1; 552/1; 1500/3; 1517/1; 1578/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C25E10.
A;Reference number: Z18376
A;Accession: T15608
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374 EDVCVPFDFCD 384
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                                                                                                                                                                        : |:|:
235 TOEECD 240
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                                                                                                                               66 SAEDCE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: C09F9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T19130
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A)Cross-references: EMBL:U50311; NID:g1226295; PID:g1226304; PIDN:AAA92314.1; CESP:C25B1
A)Experimental source: strain Bristol N2
Genetic Scores: A)Gene: CESP:C25B10.9
A;Introns: 1/3; 18/1; 41/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-137 <BRA>
A;Cross-references: EMBL:U50311; NID:g1226295; PID:g1226303; PIDN:AAA92313.1; CESP:C25E1
A;Experimental source: strain Bristol N2
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R;Okabayasahi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asashima, M.; Sugino, H. Blochem. Biophys. Res. Commun. 224, 406-413, 1996
A;Title: CDNA cloning and expression of the Xenopus laevis vitellogenin receptor. A;Reference number: JC4858; MUID:96295501; PMID:8702402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLDL receptor precursor - African clawed frog
NyAlternate names: very low density lipoprotein receptor; vitellogenin receptor
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C25B10.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ATMOCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQD-CVCEEGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPN----VPCLVRVCHQDCVCEEG
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                                                                    submitted to the EMBL Data Library, February 1996
A; Description: The sequence of C. elegans cosmid C25E10.
A; Reference number: 218376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C25E10.
A;Reference number: Z18376
A;Accession: T15609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%; Score 98.5; DB 2;
32.0%; Pred. No. 0.022;
ive 11; Mismatches 19;
                                                                                                                                                                                             A,Accession: T15610
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-135 <BRA>
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.08
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 FYRNKDDKCVSAEDC
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C; Accession: T15610
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R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A.Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro A;Reference number: 222080; MUID:98123114; PMID:9452463
A;Reference number: 222080; MUID:98123114; PMID:9452463
A;Retence number: 222080; MUID:98123114; PMID:9452463
A;Retence number: 222080; MUID:98123114; PMID:9452463
A;Rotaus preliminary; translated from GB/EMBL/DDBJ
A;Rotaus preliminary; translated from GB/EMBL/DDBJ
A;Rotaus references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1
C;Genetics:
A;Genetics:
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               급
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R; Pancer, Z.; Rast, J.P.; Davidson, E.H.
Immunogenetics 49, 773-786, 1999
A; Title: Origins of immunity: transcription factors and homologs of effector genes of A; Reference number: Z18253; MUID:99328904; PMID:10398804
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A;Molecule type: mRNA
A;Residues: 1-1036 <PAN>
A;Cross-references: EMBL:AF076513; NID:94164530; PID:94164531; PIDN:AAD05493.1
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hypothetical protein C25E10.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                           Species: Mus musculus (house mouse)

Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.6%; Score 100; DB 2; Length 5376;
Best Local Similarity 33.8%; Pred. No. 0.34;
Matches 25; Conservative 10; Mismatches 27; Indels 12; Gaps
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Best Local Similarity 26.6%; Pred. No. 0.11;
Matches 21; Conservative 13; Mismatches 21; Indels 24; Gaps
                                                                                                                                                      zonadhesin - mouse
N;Alternate names: sperm-specific membrane protein
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314 INCEYQCHQTPFGGECFCPPGHIINSNDSRTCIDFDDCQI 353
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A,Molecule type: mRNA
A,Residues: 1-4660 <SAI>
                                                                                                                                                                                                                        protein C10G8.4 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                      R_{\rm j}anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.4%; Score 94.5; DE
28.8%; Pred. No. 0.035
:ive 13; Mismatches
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hes 23; Conservative
                                                                    158 SG-CVRQRDC 166
            61 DDKCVSAEDC 70
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Best Local Similarity
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Best Local S:
Matches 23,
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A; Residues: 1-869 < CKA>
A; Residues: 1-869 < CKA>
A; Residues: 1-869 < CKA>
A; Cross-references: GB:AB006906; NID:g2366772; PIDN:BAA22145.1; PID:g2366773
C; Comment: This receptor mediates incorporation of vitellogenin into occytes c; Cymperfamily: LDL receptor mediates incorporation of vitellogenin into occytes C; Superfamily: LDL receptor; EGF homology; LDL receptor #status predicted < RAT>
F; 27-869 Froduct: VLDL receptor #status predicted < RAT>
F; 27-869 Froduct: VLDL receptor ligand-binding repeat homology < LDL2>
F; 112-148/Domain: LDL receptor ligand-binding repeat homology < LDL3>
F; 112-148/Domain: LDL receptor ligand-binding repeat homology < LDL3>
F; 112-148/Domain: LDL receptor ligand-binding repeat homology < LDL5>
F; 123-28/Domain: LDL receptor ligand-binding repeat homology < LDL5>
F; 238-272/Domain: LDL receptor ligand-binding repeat homology < LDL5>
F; 238-272/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 277-311/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 238-272/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 277-311/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 238-272/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 239-393/Domain: LDL receptor ligand-binding repeat homology < LDL7>
F; 230-250/Domain: LDL7 F; 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;794-815/Domain: transmembrane #status predicted <TMM>
F;816-869/Domain: intracellular #status predicted <CYT>
F;810-84/Region: coated-pit mediated internalization signal
F;150, 201,777,786/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;359-370,366-379,381-393,399-409,405-418,420-433,707-720,716-735,737-749/Disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:chr_V; PIDN:AAB65990.1; PID:g2315490; GSPDB:GN00023; CESP:B0238.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 QSPQRCGRNETFRTCGS-SCEPSC----TTPRPQACTMQCIVNVCQ----CSEGFVRGP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 APQRCSANEM--PCGSGECIHKKWRCDGDADCKDKSDEINCPSRTCQPDQFKCEDGNCIH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ATMOCGENEKYDSCGSKEC-DKKCKYDGVEEEDDEEPNVPCLVRVCHQD-CVCEGGFYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      < YW4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  < XW5 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <YW1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%; Score 96.5; DB 1; Length 869; 35.4%; Pred. No. 0.16; tive 8; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology
homology
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31.4%; Pred. No. 0.049;
ive 9; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology <EG1>
homology <EG2>
receptor YWTD-containing
receptor YWTD-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF homology <EG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 KDDKCVSAEDCELDNMDFI
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nes 22; Conserv
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F;526-568/Domain: L
F;569-612/Domain: L
F;613-655/Domain: L
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A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology. A; Reference number: A75000; MUID: 99069613; PMID: 9881916.
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Accession: C99046
A; Astatus: preliminary
A; Midlecule type: DNA
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S.Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:chr_V; PIDN:AAB09171.1; PID:g1572829; GSPDB:GN00023; CESP:C10G8.4 C;Genetics:
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C/Species: Rattus norvegicus (Norway rat)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPN-----VPCLVRVCHQDCVCEEGFYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 RCPSNEEFRSCGT-ACEPTC------ONPNPQVCTLQCILINVCQ----CSQGFVRG
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R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin,
A;Reference number: A58173; MUID:95024033; PMID:7937880
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-hes 17; Indels
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Chymotrypsin/elastase inhibitor - common roundworm
C;Species: Ascaris lumbricoides (common roundworm)
C;Species: Ascaris lumbricoides (common roundworm)
C;Accession: 507127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Blochem. Biochem. Biochys. 232, 143-161, 1984
Artle: The isochinibitors of chymotrypsin/elastase from Ascaris lumbricoides: the prima A;Reference number: 507127
A;Accession: 507127
A;Accession: 507127
A;Accession: 507127
A;Accession: 507127
A;Wolecule type: protein
A;Residues: 163 cBAB>
C;Superfamily: roundworm trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCE--EGFYRNKDDK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.0%; Score 92.5; DB 2; Length 63; Best Local Similarity 32.8%; Pred. No. 0.042; Matches 22; Conservative 5; Mismatches 27; Indels 13; Gaps
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54 CIPASQC 60
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Search completed: December 8, 2003, 09:19:30 Job time : 35.7879 secs

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AAG98026
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AAM53328 AAM53329 AAM45230 AAG99966 AAG99983

AAG99987 AAG99988

AAM00011 AAM00013

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AAY46652 standard; Peptide; 1 AA
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8, 2003, 09:13:30 ; Search time 5.45455 Seconds (without alignments) 116.399 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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ABU52118 ABG95255 ABG95471

ABG93483 ABG93484 ABG93489 ALIGNMENTS

		de			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB	a	Description
-	0	0.0	-	20	AAY46652	Immunogenic per
7	0	0.0	-1	22	ABB56870	Human SNP relat
٣	0	0.0	-	22	ABB66809	Drosophila mela
4	0	0.0	-	22	ABB66810	Drosophila mela
2	0	0.0	-	22	ABG02941	Novel human dia
9	0	0.0	-	22	AAM97643	Human peptide
7	0	0.0	1	22	AAM97834	Human peptide
80	0	0.0	ч	22	AAM97974	Human peptide
6	0	0.0	1	22	AAM98354	Human peptide

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01-DEC-1999 (first entry)
Immunogenic peptide having a human leukocyte antigen binding motif #1263.
Human leukocyte antigen, binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
Synthetic. Homo sapiens.
WO9945954-A1.
16-SEP-1999.
13-MAR-1998; 98WO-US05039.
13-MAR-1998; 98WO-US05039.
(EPIM-) EPIMMUNE INC.
Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
WPI; 1999-551214/46.

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AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also knowing a human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLAA subtypes (HLAA-21., A1, A3.2 or A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also used to induce a cytotoxic T cell response, by concacting a cytotoxic T cell with the peptide e.g. to broadce CTLS exive immunosenic peptides are also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
           New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SNP related amino acid sequence SEQ ID NO:1435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutically and for immunisation as above
                                                                         Claim 1; Page 80; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB56870 standard; Peptide; 1 AA.
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comprising one or more single nuclectide acts of the SNP. ABB56511 to ABB56903 represent human peptides encoded by some of the SNP coligonuclectides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimodials activities. Nucleic acids, polypeptides, oligonucleotides antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology ascribed to the presence of a sequence polymorphism. The care also useful for determining which forms of a characterised of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised of the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                 ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
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0; Mismatches
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                                Claim 1; Page 666; 674pp; English.
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11-JUL-2000; 2000US-0614150.
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sequence polymorphism
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N-PSDB; ABL10912.
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Matches
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                              Novel human diagnostic protein #2932.
                                                                                                      ABG02941 standard; Protein; 1 AA.
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS67128.
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                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL16176-ABL36511), expressed DNA
                                                                                                                                                      Gaps
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                     1; Indels
                                                                                                                            Length 1;
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                                                                                                                                                                                                                                                                                                                                            prosophila melanogaster polypeptide SEQ ID NO 27222.
                                                                                                                            Score 0; DB 22;
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Pred. No. 0;
0; Mismatches
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0; Mismatches
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                     0; Conservative
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                                     (ABB57737-ABB72072)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical
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polymetrate (II) sequences. (I) is useful as hybridisation probes, polymetrate and tor chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The color includes are also used in diagnostics as expressed sequence tags to polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical insorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in chagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and annow the angent amino acid sequences of the invention.
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invention relates to isolated polynucleotide (I) and
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0; Mismatches
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Best Local Similarity 0.0%;
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RESULT 7 AAM97834

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The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, and and anglopoletin, apoptosis related proteins, cacherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthitis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                 Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antinicrobial; gene therapy; vaccine; amylase; cancer; amylose; approtesin; appotesis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytcohrome; kinesin; cytcokine; interferon; interleukh; G-protein coupled receptor; thioseterase; inflammation; multifactorial disease; autobimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
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                                                                                                                                                             Human peptide #918 encoded by a SNP oligonucleotide.
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                                       AAM97643 standard; Peptide; 1 AA
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27-DEC-2000; 2000US-0173419.
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RESULT 6
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The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, amplotosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colons stimulating factors, complement related proteins, cycchromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptide encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with in prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
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                                                                                                                                          Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amylod protein; anglodopietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterfleukin; Grptotein coupled receptor; thioesteraes; interferon; multifactorial disease; autoimmune disease; infection; nervous system disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
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                                                                                                            Human peptide #1109 encoded by a SNP oligonucleotide.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 3911; 4143pp; English.
AAM97834 standard; Peptide; 1 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000; 2000WO-US35498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0%;
                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465210/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AA;
                                                                                                                                                                                                                                                                                                                                                          WO200147944-A2
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 X 1
                                                                           24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2001.
                                    AAM97834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RESULT 8 AAM97974

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0; Gaps

1; Indels

0.0%; Pred. No. 0; tive 0; Mismatches

1 X 1

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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; arelated protein; cacherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; multifactorial disease; autoimmune disease; inflammation; nervous system disease.

Human peptide #1629 encoded by a SNP oligonucleotide.

24-JAN-2002 (first entry)

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The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinass, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, complement related proteins, Grotein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The present sequence is a peptide encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with comparopriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases (with a genetic component, such as auttoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
                                                                                                                                                     Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; appotosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; interferon; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Grave's disease), inflammation, cancer (e.g. cancers of the blade brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 1;
                                                                                                                      Human peptide #1249 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 0; DB 2
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3941; 4143pp; English.
AAM97974 standard; Peptide; 1 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
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Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000; 2000WO-US35498
                                                                                  24-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                              WO200147944-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001
                                         AAM97974;
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Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

28-DEC-1999; 99US-0173419. 27-DEC-2000; 2000US-0173419. 28-DEC-2000; 2000WO-US35498

28-DEC-1999;

WO200147944-A2.

05-JUL-2001.

Homo sapiens

(CURA-) CURAGEN CORP.

Leach M;

Shimkets RA,

WPI; 2001-465210/50.

Disclosure; Page 4025; 4143pp; English.

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The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, anglopoiethn, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytchromes, kinasins, cytckines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with in the prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arbitis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1;
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Pred. No. 0;
0; Mismatches
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1; Indels

ò 셤 AAM98354 standard; Peptide; 1 AA.

RESULT 9 AAM98354 AAM98354

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Gaps ; 0

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protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic.
                                                                        WO200140521-A2
                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                             therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, anglopolettin, apptrosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cycokines, complement related proteins, cycokines, complement related proteins, cycrotein coupled receptors and thioesterases. The present sequence is a peptide encoded by them may be used in the prevention, diagnosis and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthitis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's adisease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                         Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nonconservative amino acid changing SNP related peptide SEQ:6913.
                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; single nucleotide polymorphism; SNP; genome; gene therapy;
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   Human peptide #1722 encoded by a SNP oligonucleotide.
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iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 4045; 4143pp; English.
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                                                                                                                                                                                                                                                                               28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                        Shimkets RA, Leach M;
                                                                                                                                  nervous system disease
                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                            WO200147944-A2.
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                                                                                                                                                                Homo sapiens
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ID AAM!
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AAT73060 to AAT79867 represent isolated human polymorphic polynuclectide sequences (I), which contain single nuclectide polymorphisms (SNPs).
AAM53134 to AAM53329 represent peptides related to human polymorphic conjunction by a sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by therapy, and in vaccine production. (I) and the polypeptides encoded by the may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides.
Cor example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be used as antigens in the production of antibodies encoded by (I) may be used as antigens in the antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human nonconservative amino acid changing SNP related peptide SEQ:6914.
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                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic nucleic acid sequences, useful in genetic testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0%; Pred. No. 0; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Page 2619; 2653pp; English
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                                                                                                                       30-NOV-1999; 99US-0168138.
29-NOV-2000; 2000US-0726173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.08;
                                                          30-NOV-2000; 2000WO-US32758.
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                                                                                                                                                                                                                                                                           Shimkets RA, Leach M;
                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                            WPI; 2001-356160/37
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Best Local Similarity
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07-JUN-2001
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Shimkets RA,
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                                                                                                              therapy
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AAM53291
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                                                                                                                                                                                                                                                            character to numan polymorphic pepties related to numan polymorphic polymucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides.

For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The matibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                              AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs) AAW53114 to AAW53129 represent peptides related to human polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nonconservative amino acid changing SNP related peptide SEQ:6985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                  Polymorphic nucleic acid sequences, useful in genetic testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 0; DB 22; Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                      Claim 29; Page 2619; 2653pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.08;
                                   30-NOV-2000; 2000WO-US32758
                                                         30-NOV-1999; 99US-0168138
29-NOV-2000; 2000US-0726173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Conservative
                                                                                                                      Leach M;
                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                           WPI; 2001-356160/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AA;
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                                                                                                                   Shimkets RA,
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           07-JUN-2001
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AA173660 to AA179867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNBs).

AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides.

For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be used as artigens in the therapy. The polypeptides encoded by (I) may be used as artigens in the antibodies may also be used as diagnostic agents for detecting the antibodies may also be used as diagnostic agents for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nonconservative amino acid changing SNP related peptide SEQ:6986.
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                                                                                                                                                                                                                                                                                               Polymorphic nucleic acid sequences, useful in genetic testing and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       presence of polymorphic polypeptides in samples
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; Page 2641; 2653pp; English.
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29-NOV-2000; 2000US-0726173.
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29-NOV-2000; 2000US-0726173.
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Best Local Similarity 0.0%
Matches 0; Conservative
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                                                                        (CURA-) CURAGEN CORP.
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                                                                                                                                                 Shimkets RA,
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AM53114 to AAM53329 represent reptides related to human polymorphisms (SNPS).

AM53114 to AAM53329 represent peptides related to human polymorphism (SNPS).

AM53114 to AAM53329 represent peptides related to human polymorphic polymorphic polymorphic polymorphic polymorphic polymorphic protein the prevention. (I) and the polymorphic polymorphic protein them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic production of polymorphic presence of polymorphic polymorphic as adapted the antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polymorphic polymorphic polymorphic polymorphic polymorphic polymorphic production the presence of polymorphic po
                                                                                                                                                                    represent isolated human polymorphic polynucleotide
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protein therapy; vaccine; probe; diagnostic assay; detection;
quantitation; restorative therapy; polymorphic.
                                                Polymorphic nucleic acid sequences, useful in genetic testing and
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                                                                                                                       Claim 29; Page 2641; 2653pp; English
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29-NOV-2000; 2000US-0726173.
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Query Match
Best Local Similarity 0.0%;
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                                                                                                                                                                       AAI73060 to AAI79867
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WPI; 2001-356160/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AA;
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associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polymorphic polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.
                           polymorphic polynucleotide
                    AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (1) which contain single nucleotide polymorphisms (SNPB). AAM531314 to AAM53129 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (1) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases
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1 AA; Seguence

Gaps ö Indels Score 0; DB 22; Length 1; ۲; Pred. No. 0; 0; Mismatches 0.0%; 0.0%; F 0; Conservative Best Local Similarity Matches 0; Conserv Query Match

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Search completed: December 8, 2003, 09:16:39 Job time : 5.45455 secs

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                               Q8G112 Q8G112 Q8G112 Q8G104 Q8
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Last annotation update)
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4 AA; 473 MW; 633732C42000000 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update
Bilirubin UDP-glucuromosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 0; DB 11;
Pred. No. 0;
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P83073
ID P83073 PRELIMINARY; PRT;
AC P83073; DT 01-OCT-2001 (TrEMBLrel. 18, Created)
034028
007354
007354
08GL12
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P92218
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Q99007 hordeum vul
P83189 gallus gall
P82181 spinacia ol
P82182 spinacia ol
P82182 spinacia ol
Q87182 scherichia
Q47505 escherichia
Q47477 escherichia
Q47477 escherichia
Q47629 enterobacter
P72081 nocazdia la
Q5448 streptomyce
Q64489 enterobacte
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            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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Q9907
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Gapop 10.0 , Gapext 0.5
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Gaps

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1; Indels

Score 0; DB 13; Length 5;

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Dockray G.J., "keeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.; "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide."; Nature 305:328-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
                                                                                                                                                                                                                                                                        5 AA; 645 MW; 69D4073767400000 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0;
0; Mismatches
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Matches 0; Conserv
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les 0; Conserv
TISSUE=Brain;
PubMed=6137771;
                                                                                                                                                                                                                                               Neuropeptide.
SEQUENCE 5
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=91329704; PubMed=1831055;
MEDLINE=91329704; PubMed=1831055;
Macobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature bareley aleurone layers.";
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                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBL_TaxID=1396;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FMRFanide-like neuropeptide (LPLRF-amide).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                   SEQUENCE.
STRAIN=NCIMB 11796;
STRAIN=NCIMB 11796;
Submitted (JUL-2001) to the SWISS-PROT data bank.
NON TER
SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
(TrEMBLrel. 18, Last sequence update) (TrEMBLrel. 18, Last annotation update)
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Pred. No. 0;
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EMBL; X54643; CAA38455.1; -.
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Guery Match
Best Local Similarity 0.0*;
Best Local Similarity
0; Conservative
                                                      88 kDa protein (Fragment)
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Best Local Similarity 0.0*
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                                                                                     Bacillus cereus.
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SEQUENCE
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MEDLINE=20435798; PubMed=1087464;

MEDLINE=20435798; PubMed=10874646;

A menguchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 275:28466-28482(2000).

- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 238 RIBOSOMAL RNA.

- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 238 RIBOSOMAL RNA.

- I SUBCELLULAR LOCATION: CHLOROPLAST.

- I SUBCELLULAR LOCATION: CHLOROPLAST.

- I SIMILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.

InterPro; IPRO01790; Ribosomal Lilo.

R RIBOSOMAL LIO.; PARTIALL.

R RIBOSOMAL PROOFEST.

R RIBOSOMAL LIO.; PARTIAL.

R RIBOSOMAL PROCEIN; CHLOROPLAST.

R RIBOSOMAL PROCEIN; CHLOROPLAST.

R RIBOSOMAL PROCEIN; CHLOROPLAST.

R RIBOSOMAL PROCEIN; CHLOROPLAST.

R RIBOSOMAL PROCEIN; CHLOROPLAST.
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                                                                                                                                                                                                         Spinacia oleracea (Spinach).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

NCBI TaxID=3562;
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                                                                01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 17, Last annotation update)
Chloroplast 30S ribosomal protein S19 beta (Fragment).
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6 AA.
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tive 0; Mismatches
PRT;
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Gaps

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SEQUENCE FROM N.A.
MEDLINE=9609297; PubMed=8522520;
Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
Gonzalez-Pastor J.E., San Millan J.L.,
Structure and organization of plasmid genes required to produce the translation inhibitor microcin C7.";
J. Bacteriol. 177:7131-7140(1995).
Plasmid. X57583; CAA40808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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"Mercury resistance transposons of Gram-negative environmental bacteria and their classification.";
Res. Microbiol. 152:811-822(2001).
ERBL; AJ302776; CAC82975.1;
SEQUENCE 7 AA; 608 MW; 6DC1BSBDD87DD6F0 CRC64;
                                      1; Indels
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  Length 6;
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  DB 10;
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                                    Mismatches
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Pred. No. 0;
0; Mismatches
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Matches 0; Conservative 0; Mismatches
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NCBI_TaxID=143776;
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                    0.0%;
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Query Match 0.0
Best Local Similarity 0.0%
Matches 0; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q8KMS3
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                                                                                                                             STRAIN=cv. ALWARO; TISSUE=Leaf;
MEDLINE=20435798; PubMed=10874046;
Yamaquchi K., Subramanian A.R.;
"The plastid ribosomal proteins Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28466-28482(2000).
-I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               -: SUBCELLULAR LOCATION: CHLORPLAST.
-: TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
-: MASS SPECIFORETRY: MW=10477.0; METHOD=ELECTROSPRAY.
-: MASS SPECIFOMETRY: MW=10495, METHOD=MALDI.
-: MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA FORM IS THE MINOR BASIC FORM.
-: MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
-: MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
-: SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
InterPro; IPR002222; Ribosomal_S19.
PFEMI; PF00203; Ribosomal_S19; PARTIAL.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllidae, Caryophyllales, Chenopodiaceae; Spinacia.
VCBI_TaxID=3562;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
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-i- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
-i- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
-i- SIMILARITY: BELONGS TO THE LIUP FAMILY OF RIBOSOWAL PROTEINS.
InterPro; IPR001790; Ribosomal Li0.
Pfan: PF00466; Ribosomal Li0.
PROSITE; PS001109; Ribosowal Li0; PRATIAL.
RIBOSOMAL Li0; PRATIAL.
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RRIBOSOMAL LI0; PRATIAL.
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
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Ribosomal protein; Chloroplast; rRNA-binding.
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                                                                                                             SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
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PRINTS; PR00975; RIBOSOMALS19; PARTIAL
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SECUENCE FROM N.A.
MEDLINE=94079349; PubMed=8257126;
MEDLINE=94079349; PubMed=8257126;
MEATHER P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-VIa gene encoding a novel 3-N-
acetyltransferase.";
Antimicrob. Agents Chemother. 37:2074-2079(1993).
EMBI: M88012; AAA16193.1; -.
NON_TER
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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MEDLINE=85203917; PubMed=3158524;
Hellinga H.W., Evans P.R.;
"Nucleotide sequence and high-level expression of the major
Escherichia coli phosphofructokinase.";
Eur. J. Biochem. 149:363-373(1985).
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Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X02519; CAA26359.1;
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"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algg) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL; X87973; CAA61230.1; -.
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Infect. Immun. 64:3451-3460(1996).
EMBL; US1862; AAB88721.1; -.
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MEDLINE-96355846; PubMed=8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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MEDLINE=96009872; Pubmed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liraa P.;
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STRAIN-N2-3-11;
MEDLINB-20011291; PubWed=10542330;
Poehling S., Piepersberg W., Wehmeier U.F.;
Poehling S., Piepersberg W., Wehmeier U.F.;
N2-3-11 and interaction of the sec Y grotein with the SecA protein.";
Biochim. Biophys. Acta 1447:298-302(1999).
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1911;
                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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0.0%; Pred. No. 0;
tive 0; Mismatches 1; Indele
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0.0%; Pred. No. 0;
tive 0; Mismatches 1; Indel
                                                                           Last sequence update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
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                                7 AA.
                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequent
01-DEC-2001 (TrEMBLrel. 19, Last annotat
3.-methylcephem hydroxylase (Fragment).
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Matches 0; Conservative
                             PRELIMINARY;
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Best Local Similarity 0.09
Matches 0; Conservative
                                                                                                                                   Nocardia lactamdurans.
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Q54248;
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Q54248
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Copyright (c) 1993 - 2003 Compugen Ltd.
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December 8, 2003, 09:13:30 ; Search time 1.05051 Seconds (without alignments) 179.063 Million cell updates/sec

US-09-498-556C-85 Title: Perfect score: Sequence:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		· de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
-	0	0.0	 M	<u>:</u> -	GRWM HUMAN	P01157 homo sapien
7	0	0.0	m	-	LUXE_VIBFI	P24272 vibrio fisc
e	0	0.0	m	٦	THYL_PIG	P01151 sus scrofa
4	0	٠	4	н	ACH1_ACHFU	P35904 achatina fu
'n	0	0.0	4	н	DCML_PSECH	P19916 pseudomonas
φ	0	0.0	4	-	DCMS_PSECH	P19918 pseudomonas
7	0	0.0	4	-	EOSI HUMAN	P02731 homo sapien
80	0	0.0	4	Н	FAR3 HIRME	P42562 hirudo medi
σ	0		4	П	FAR4_HIRME	P42563 hirudo medi
10	0		4	г	FFKA ANTEL	P58705 anthopleura
11	0	•	4	ч	FLRF HIRME	
12	0		4	ч	FLRN ANTEL	P58707 anthopleura
13	0	٠	4	ч	FMRF MACNI	~
14	0		4	٦	FYRI_ANTEL	P58706 anthopleura
15	0		4	ч	OCP1_OCTMI	P58648 octopus min
16	0	•	4	ч	OCP3_OCTMI	P58649 octopus min
17	0		4	-	RM01_YEAST	P36515 saccharomyc
18	0	0.0	4	-	TUFT_HUMAN	P01858 homo sapien
19	0		ഗ	ч	AL14_CARMA	P81817 carcinus ma
20	0		ស	Н	BIOA_CITFR	P13071 citrobacter
21	0		ស	-	BIOB_CITFR	7
22	0		ហ	-	BPP7_BOTIN	_
23	0		S	Н		
24	0		'n	-	EI04_LITRU	P82100 litoria rub
25	0		υ	٦	FARP_ARTTR	-
56	0		S	٦		4
27	0		Ŋ	Н	PRCT_PERAM	P01373 periplaneta
28	0	•	'n	Н	n	
29	0		Ŋ	-	RE11_LITRU	
30	0		S	-		н
31	0		'n	Н	RE31_LITRU	7
32	0	0.0	S	-		P82073 litoria rub
33	0	0.0	ហ	٦	SUGA_ACHDO	P19991 acheta dome

P54714 canis famil P13973 escherichia P80628 zea mays (m P38639 mus musculu P38005 chlamydia t P25154 oryccolagus P82655 lactobacill P13736 mytilus edu P82096 litoria rub P41966 moniezia ex P41491 locusta mig				ebrata; Euteleostomi; mninidae; Homo.	d-histidyl-lysine.";	BEEN FOUND TO STIMULATE OTHER TYPES IN VITRO. NAS. CRC64;	Length 3; 1; Indels 0; Gaps 0;				.) .igase (EC 6.2.1.19) (Acyl-	a; Vibrionales;	Meighen B.A.; des a bidirectional termination	ACCETION: 1/2:097-692(1590). FUNCTION: ACYL-PROTEIN SYNTHERASE ACTIVATES TETRADECANOIC ACID. IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
5 1 TPIS_CANFA 5 1 TRM3 ECOLI 5 1 UC22_MAIZE 5 1 UK02 MOUSE 5 1 UX44_CHLTR 6 1 ACPH_RABIT 6 1 ASP2_LACSN 6 1 CIPI_WYTED 6 1 CIPI_WYTED 6 1 EIOI_LITRU 6 1 FARP MONEX 6 1 LOKI_LOCMI	ALIGNMENTS	STANDARD; PRT; 3 AA.	(Rel. 01, Created) (Rel. 01, Last sequence update) (Rel. 01, Last annotation update) ating peptide.	U. Chordata, Craniata, Vertebrata, I Primates, Catarrhini, Hominidae,	SEQUENCE. MEDLINE=77162369; PubMed=858356; Schlesinger D.H., Pickart L., Thaler M.M.; "Growth-modulating serum tripeptide is glycyl-histidyl-lysine." Experientia 33:324-325(1977)	: THIS SERUM TRIPEPTIDE HAS E CELL TYPES AND TO INHIBIT :regulation of cell growth; 340 MW; 6331E81000000000 C	0.0%; Score 0; DB 1; 0.0%; Pred. No. 0; ative 0; Mismatches			STANDARD, PRT, 3 AA.	1, Last sequence update) 4, Last annotation update) idluciferin-component ligase (Fragment).	Duar. Vibrio fischeri. Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales Vibrionaceae; Vibrio. NCBI_TaxID=668;	.F., reced	17/2:6/7-6802.11990). ACYL-EROTEIN SYNTHETASE ACTIVA. OMPONENT OF THE FAITY ACID REDU YIING TETRADECANOIC ACID TO THE
33.33.33.33.33.33.33.33.33.33.33.33.33.		JT 1 HUMAN GRWM HUMAN	21-JUL-1986 (Rel. 0 21-JUL-1986 (Rel. 0 21-JUL-1986 (Rel. 0 21-JUL-1986 (Rel. 0 Growth-modulating p	Homo Bapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	SEQUENCE. MEDLINE=77162369; P Schlesinger D.H., P "Growth-modulating Experientia 33:324-	-!- MISCELLANEOUS: GROWTH OF SOME GO; GO:0001558; P:r SEQUENCE 3 AA; 3	Query Match Best Local Similarity Matches 0; Conserva	1 X 1	1 G 1	2 13BI UXE_VIBFI 24272; 1-MAR-1992 (Re	01-MAR-1992 (Rel. 2 01-OCT-1996 (Rel. 3 Long-chain-fatty-ac protein synthetase)	DOAD: Vibrio fischeri. Bacteria; Proteobac Vibrionaceae; Vibri NCBI_TaxID=668;	[1] SEQUENCE FROM N.A. MEDLINE=91072226; Pubmed=2254256; Swartzman E., Kapoor S., Graham A. "A new Vibrio fischeri lux gene p. site for the lux operon.";	J. Bacteriol. 172:6 -!- FUNCTION: ACYL- IT IS A COMPONE FOR CONVERTING
		₽.₹			R R R R R R R L R L	20 8 8 8	Out Ber Mat	ò	qa	RESULT LUXE V ID L AC P DT 0	56666	88888	RN RR RR RT	3888

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P35904;
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ACH1_ACHFU
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stimulating hormone releasing factor of ovine origin by means of mass
                  CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
PATHWAY: Bioluminescent fatty acid reduction system; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=70039904; PubMed=4982117;
Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
"The identity of chemical and hormonal properties of the thyrotropin realeasing hormone and pyroglutemyl-histidyl-proline amide.";
Biochem. Biophys. Res. Commun. 37:705-710(1969).
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Thyrollberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
Sus scrofa (Pig),
Ovis arise (Sheep),
Bombina orientalis (Oriental fire-bellied toad), and
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria, Ceratiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Sheep; TISSUE-Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
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MEDILNE=70163386; Pubmed=4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
Guillemin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=Pig; TISSUE-Hypothalamus;
MEDLINE=70136150; PubMed=4984938;
Nair. R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
"Structure of porcine thyrotropin releasing hormone.";
Biochemistry 9:1103-1106(1970).
SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
                                                                                                                                                                                                                                                                                                                                                      3 AA; 374 MW; 6AA330300000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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0; Mismatches
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0.0%; Pred No.
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Org. Mass Spectrom. 5:221-228(1971)
                                                                                                                                                                                                                                                                                     EMBL; M62812; -; NOT_ANNOTATED_CDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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tes 0; Conserv
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SPECIES=N.viridescens;
MEDLINE=75035605; PubMed=4214528;
MEDLINE=75035605; PubMed=4214528;
Grimm-10-regensen Y., McKelvy J.F.;
Grimm-10-regensen Y., McKelvy J.F.;
Haidescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
J. Neurochem. 23:471-478(1974).
J. Neurochem. 23:471-478(1974).
IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achatina fulica (Giant African snail).
Eukaryota, Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=8927351; PubMed=2597281;
Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Acharin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; "Purification of achatin-I from the atria of the African giant snail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY.
MEDLINE=93014529; PubMed=1399265;
Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                               "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID. AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Biochem. Biophys. Res. Commun. 177:847-853(1991)
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amidation; Pyrrolidone carboxylic acid.
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                                                                                                               SPECIES=B.orientalis; TISSUE=Skin;
MEDLINE=76138399; PubMed=815011;
Yasuhara T., Nakajima T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91264856; PubMed=1675568;
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TSH-releasing factor.";
Nature 226:321-325(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Conservative
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PIR; A92971; A92971.
PIR; A93750; RHSHT.
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Best Local Similarity
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01-JUN-1994
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dehydrogenase subunit S) (CO-DH S) (Fragment)
                                                                                         Bradyrhizobiaceae.
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21-JUL-1986 (Rel.
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                                                                                                        NCBI_TaxID=290;
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                                                                             Int. J. Pept. Procein Res. 39:258-264(1992).
-1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
HEART BRAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
PIR; A32480; A32480.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- COFAČTOR: Molybdenum (molybdopterin).
-i- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152:135-341(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
Iwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin-I
(H-Giy-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                      Score 0; DB 1; Length 4;
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4 AA; 408 MW; 6AADD9C810000000 CRC64;
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0; Mismatches
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                                                                                                                                                                                                                                                                                   0.0%;
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                                                              D-amino acid residue."
                                                                                                                                                                                                      Hormone; D-amino acid.
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tes 0; Conserv
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Matches 0; Conserv
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P19916;
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P19918;
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DCMS_PSECH
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Matches
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acceptor.
-!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                    MEDLINE=90055678; PubMed=2818128;
Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                    carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sāpiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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                   Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                             PIR; PL0146; PL0146.
Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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/FIId=VAR 005201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA; 420 MW; 6DD33DD6F000000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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Last annotation update)
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0; Mismatches
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MEDLINE=76078412; PubMed=1060093;
Pseudomonas carboxydohydrogena
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Eosinophilotactic peptides.
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Matches 0; Conservative
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SEQUENCE

SOCCERTARY SOCCERTARY

Query Match

Matches

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4 4 AA; 582 MW; 69D40729A000000 CRC64;
28-FEB-2003 (Rel. 41, Last annotation update)
Antho-KAamide.
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MEDLINE=94286417; PubMed=7912428;
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                                                                                          SEQUENCE.
MEDLINE=92028852; PubMed=1681803;
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MOD RES 4 4
SEQUENCE 4 AA; 582 MW;
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Neuropeptide; Amidation.
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les 0; Conserv
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                                                                                                                                                                                               MEDLINE=92195954; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Identification of RPamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech.";
                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annocation update)
01-NOV-1995 (Rel. 32, Last annocation update)
FMRFamide-like neuropeptide YLRF-amide.
Hirudo medicinalis (Medicinal leech).
Bukaryota: Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformee; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirudo medicinalis (Medicinal lech).

Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

Arynchobdellida; Hirudiniformea; Hirudinidae; Hirudo.
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SEQUENCE 4 AA; 616 MW; 69D4068B3000000 CRC64;
                                                                                                                                                                                                                                                                                           4 4 AMIDATION.
4 AA; 598 MW; 69D4073B30000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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(Rel. 41, Last sequence update)
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0; Mismatches
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                                       PRT;
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ilarity 0.0%; F
Conservative 0
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                                       STANDARD;
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es 0; Conserv
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P42563;
01-NOV-1995 (
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28-FEB-2003
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P58705;
                          FAR3_HIRME
ID FAR3_HIRME
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SEQUENCE
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FAR4_HIRME

RESULT 9

SEQUENCE

Query Match

Matches

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RESULT 10 FFKA ANTEL

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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M., "FWRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93391436; PubMed=8397415;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92195954; PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P., rainenarikhuijzen C.J.P., raineolation of L.3-phenyllactyl-phe-Lyg-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones "; Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helisoma trivolvis (Snail).
Bukaryota, Meteazoa, Annelida; Clitellata, Hirudinida; Hirudinea,
Arynchobdellida; Hirudiniformes, Hirudinidae; Hirudo.
NCBI_TaxID=6421, 27815;
Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Pred. No. 0;
0; Mismatches 1; Indels
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6DD339C9A0000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FLRFamide.
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SPECIES=M.nimbosa; TISSUE=Ganglion;
MEDLINE=78012038; PubMed=909875;
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                                                                                        SPECIES=N.virens;
                                                                                                                                                                                                                                                                                                                                                                   PIR; A01426; ECNK.
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                                                                                                                                                                                                                                                  SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=90319122; PubMed=1973541;
Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
Reinscheid R.K., Nothacker H.-P., Staley A.L.;
"Isolation of L-3-phenyllacty1-Leu-Arg-Aan-NH2 (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nereis virens (Sandworm),
Hirudo medicinalis (Medicinal leech), and
Helisoma trivolvis (Snail).
Eukaryota, Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Veneroidea; Veneridae; Macrocallista.
NCBI_TAXID=6594, 6353, 6421, 27815;
                                                                                                                                                                                         Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion; MEDLINE=77215956; PubMed=877582;
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"Structure of a molluscan cardioexcitatory neuropeptide.";
Science 197:670-671(1977).
                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
           Length 4;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1998 (Rel. 36, Last annotation update)
FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
Macrocallista nimbosa (Sun-ray clam),
                                                                                                                                                                                                                                                                                                                                                                                                 1 1 L-3-PHENYLLACTYL.
4 4 AMIDATION
4 AA; 549 MW; 64540729A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-1 SUBCELLULAR LOCATION: Secreted.
-1 TISSUE SPECIFICTY: Nouron-specific.
-1 MASS SPECIFICATY: NW=549.3; METHOD=FAB.
                                                                                                                                                   (Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
          DB 1;
      Score 0; DB 1;
Pred. No. 0;
0; Mismatches
                                                                                                                                4 AA.
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SEQUENCE, AND CHARACTERIZATION.
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        0.0%;
                   0.08
                               0; Conservative
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      Query Match
Best Local Similarity
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Best Local Similarity
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28-FEB-2003
15-SEP-2003
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P58707;
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SEQUENCE
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Price D.A., Greenberg M.J.;
"Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc.";
Prep. Biochem. 7:261-281(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=H.trivolvis; TISSUE=Kidney;
MEDLINE=94286417; PubMed=7912428;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trivolvis.";
Peptides 15:31-36(1994).
-!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-93391436; PubMed-8397415;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
                                                                                                                                                         MEDLINE=90259866; PubMed=2342992;
Krajniak K.G., Price D.A.;
"Authentic PMRFamide is present in the polychaete Nereis virens.";
Peptides 11:75-77(1990)
                                                                                                                                                                                                                                                                                                  SPECIES-H.medicinalis;
MEDLINE-S2195954, PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
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Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
Grimmelikhuijzen C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 4 4 AMIDATION.
4 AA; 600 MW; 69D40699A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 0; DB 1;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Antho-RIamide I [Contains: Antho-Riamide II].
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[5]
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Neuropeptide; Amidation.
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28-FEB-2003 (Rel. 41, Last sequence update).
28-FEB-2003 (Rel. 41, Last annotation update).
Cardioactive peptides Ocp-1/Ocp-2.
Octopus minor (Octopus).
Eukaryota; Metaco; Mollusca; Cephalopoda; Coleoidea; Neccoleoidea; Octopodiformes; Octopodi Incirrata; Octopodidae; Octopus.
NCBL TaxID=89766;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
Neuropeptide; Amidation.
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                                                                                                                                                                                                  Score 0; DB 1; Length 4;
                                                                                                                    ANTHO-RIAMIDE I.

ANTHO-RIAMIDE II.

ANTHO-RIAMIDE II.

L-3-PHENYLLACTYL.

AMIDATION.

AMIDATION.

AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 D-PHENYLALANINE.
4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    active than Ocp-1.
-!- SUBCELLUAR LOCATION: Secreted.
-!- PTW: Ocp-2 has L-Phe instead of D-Phe.
-!- PTW: Ocp-2 has L-Phe instead of D-Phe.
-!- MASS SPECTROMETRY: WW=395.2; METHOD=MALDI.
MOD_RES.
2
2
D-DHPMANTATATATATATA
                                                                                                                                                                                                             Local Similarity 0.0%; Pred. No. 0; nes 0; Conservative 0; Mismatches
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tive 0; Mismatches
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Matches 0; Conservative
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Search completed: December 8, 2003, 09:14:14 Job time : 2.05051 secs

5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2003

OM protein - protein search, using sw model

December Run on:

8, 2003, 09:13:30 ; Search time 1.65657 Seconds (without alignments) 232.212 Million cell updates/sec

US-09-498-556C-85

1 XXXX 4 Title: Perfect score: Sequence: Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

rip	thyroliberin - Bom	1	1	1	growth-modulating	bursin - chicken	spinal cord peptid	cord	thyrotropin-releas	R-phycoerythrin al	angiotensin-conver	histidinol dehydro	TRH-like tripeptid	bradykinin-potenti	bradykinin-potenti	gene p20K protein	T-cell receptor be			T-cell receptor be	tyrosine protein k	blood cell protein	cytochrome-c oxida	antho-RFamide neur	thyroglobulin - do	phagocytosis-stimu	tyrosine-melanocyt	cardioexcitatory n	carbon-monoxide de
ID	RHTDTO	RHPGT	RHSHT	A92971	GKHU	A60898	A23751	B23751	A33802	A22565	PQ0010	S13894	A43391	E37196	F37196	I50412	PT0636	PT0578	PT0571	PT0622	178890	S68328	T13892	ECXAA	S18401	A02147	A32039	ECNK	PL0140
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PL0146 A27832 A48360 I40697 A61300 I57745 A41890 A41890 B43848 I40505 I40870 I40804 T46627	S17255
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ALIGNMENTS

RESULT 1

thyroliberin - Bombina orientalis

Cipecies: Bombina orientalists
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cipate: 15-Jun-2001
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A;Reference number: A90919; MuID:76138399; PMID:815011
A;Accession: A90919
A;Accession: A90919
A;Accession: A90919
A;Accession: Aspertantly precursor
C;Superfamily: thyroliberin precursor
C;Superfamily: thyroliberin precursor
C;Superfamily: thyroliberin carboxyle acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxyle acid (Gln) #status experimental

ö Length 3; DB 3; Query Match 0.0%; Score 0; DB 3
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches

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Gaps

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Libroliberin - pig C;Species: Sus scrofa domestica (domestic pig) C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001 C;Accession: A01415 C;Accession: A01415 B;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V. Biochemistry 9, 1103-1106, 1970 A;Tille: Structure of porcine thyrotropin releasing hormone. A;Rille: Structure of MUID:70136150; PMID:4984938

A;Accession: A01415 A;Molecule type: protein A;Residues: 1-3 <NAI>

R;Boler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
Biochem. Blopbys. Res. Commun. 37, 705-710, 1969
A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing lA;Reference number: A90167; MUID:70039904; PMID:4982117

A; Contenns: annotation A; Note: biological activities and Rf values (in 17 chromatographic systems) of the synth

C.Superfamily: thyroliberin precursor C.Keywords: amidated carboxyl end, hormone; hypothalamus; pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;3/Modified site: amidated carboxyl end (Pro) #status experimental

0.0%; Score 0; DB 3; Length 3; Query Match

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A, Accession: A01421
A, Molecule type: protein
A, Residues: 1-3 < SCH>
A, Note: this serum tripeptide is found to stimulate growth of some cell types and to inh:
C, Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiAudhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 21, 997-999, 19866
A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of tl
A;Reference number: A60899; MUID:86122916; PMID:3484838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A60898
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Species: Homo sapiens (man)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001
C;Accession: A) 40421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experiantla 33, 324-325, 1977
Experiantla 33, 324-325, 1977
A;Tile: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
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A;Molecule type: protein
A;Residues: 1-3 <AUD>
C;Superfamily: unassigned animal peptides
C;Superfamily: unassigned animal hormone
C;Keywords: amidated carboxyl end; hormone
F;3/Modified site: amidated carboxyl end (Gly) #status experimental
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tive 0; Mismatches
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C;Superfamily: unassigned animal peptides
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Matches 0; Conservative
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A, Molecule type: protein
A, Residues: 1-3 <HSI>
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (castern newt)
C;Date: 15-30n-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A92971; A01415
R;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) bra
A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Residues: 1-3 <GRI>
A;Notecule type: procein
A;Notecule type: procein
C;Superfamily: thyroliberin precursor
C;Superfamily: thyroliberin precursor
C;Superfamily: thyroliberin precursor
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic
C;JNodified site: pyrrolidone carboxyl end (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: protein
A, Residues: 1-3 < DES>
A, Residues: 1-3 < DES>
B, Surgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A, Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A, Reference number: A93161; MUID:70163386; PMID:4985794
A, Contents: annotation
A, Note: physicochemical characteristics and biological activities of the natural and syn
C, Superfamily: thyroliberin precursor
C, Superfamily: thyroliberin precursor
C, Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                       C; Species: Ovis Orientalis aries, Ovis ammon aries (domestic sheep)
C; Species: Ovis Orientalis aries, Ovis ammon aries (domestic sheep)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession Jr., D.M.; Burgus, R., Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
Org. Mass Spectrom. 5, 221-228, 1971
A; Title: The elucidation of the primary structure of the hypothalamic thyroid stimulatin A; Accession: A93750
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Matches 0; Conservative 0; Mismatches
  Pred. No. 0;
0; Mismatches
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R,Lackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391, MUID:92388092; PMID:1517203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Distriction dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Species: Brassica oleracea (wild cabbage)
C;Dacession: S13894
R;Nagai, A.; Scheidegger, A.
Arch. Blochem. Biophys. 28, 127-132, 1991
Arch. Brochem. Biophys. 28, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: S13894; MUID:91112783; PMID:1989490
                                                                                                                                                                      R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. S3, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
                                                   angiotensin-converting enzyme inhibitor (FLP-3) - common fig
NyAlternate names: ficus latex peptide 3
C.Species: Ficus carica (common fig)
C.Species: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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C,Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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100.0%; Pred. No. 0;
tive 0; Mismatches
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0; Mismatches
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A;Residues: 1-3 «NAG»
Experimental source: var. capitata
C;Keywords: dimer; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                              0.0%;
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Best Local Similarity 0.0%;
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                                                                                                                                                                                                                                                                A;Accession: PQ0010
A;Molecule type: protein
A;Residues: 1-3 <MAR-
A;Estimental source: latex
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A;Molecule type: protein
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Matches 1; Conserv
                                                                                                                                                    C; Accession: PQ0010
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A33602
R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
J. Biol. Chem. 264, 7788-7791, 1989
A;Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate comp A;Reference number: A33802; MUD:89255196; PMID:2498305
A;Accession: A33802
A;Accession: A33802
A;Reterence number: A33802
A;Reterence number: A33802
A;Reterence number: A33802
C;Superfaminary
A;Molecule type: protein
A;Residues: 1-3 <COC>
C;Superfamily: unassigned animal peptides
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxyl end (Pro) #status experimental
                                                               C. Accession: B23751
R.Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, A.Hsi, K.L.; Chen, R.L.; Chen, B. 178-183, 1985
A.Accession: B23751
A.Accession: B23751
A.Status: preliminary
A.Status: preliminary
A.Nolecule type: protein
A.Residues: 1-3 -4815
C.Superfamily: unassigned animal peptides
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'Species: Sus scrofa domestica (domestic pig)
'Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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Best Local Similarity 0.0%;
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Figure 1.3

Figure 1.3

Figure 1.3

States 1.5 - Jun-2001 #sequence_revision 15 - Jun-2001 #text_change 15 - Jun-2001

C, Species Bothrops insularis (island jararaca)

C, Species Bothrops insularis (island jararaca)

C, Species Bothrops insularis (island jararaca)

C, Accession: F37196

R; Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A; Title: Primary structure and biological activity of bradykinin potentiating peptides !

A; Reference number: A37196, MUID:90351557; PMID:2386615

A; Reterence type: protein

A; Residues: preliminary

A; Molecule type: protein

A; Residues: 1-3 < CIN>

C; Keywords: pyroglutamic acid

E; I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                   RESULT 14
B27196
bradyVinin-potentiating peptide 5 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
J. Protein Chem. 9, 221-227, 1990
A;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Atcession: B7196
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: E37196
A;Accession: E37196
A;Accession: B7196
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Reference number: A37196
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Reference number: A37196; PMID:2386615
A;Reference number: A37196; PMID:2386615
A;Reference number: A37196; PMID:2386615
A;Reference number: A371
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Sequence 2, A
Sequence 3, A
Sequence 4, A
Sequence 5, A
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APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Tuan, Tai-Lan
APPLICANT: W. Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 9; DB 1; Length 3; 66.7%; Pred. No. 2.5e+05; ive 0; Mismatches 1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
US-08-392-973A-9

US-08-477-1342-173

US-08-892-544-173

US-08-473-489A-173

US-08-485-695-173

US-08-485-695-173

US-09-246-500B-173

US-09-367-791A-108

5464756-42

US-08-367-731A-108

5464756-42

US-08-33-724-35

US-08-236-427-11

US-07-923-724-35

US-08-806-203-3

US-08-806-203-3

US-08-806-203-4

US-08-806-203-4

US-08-806-203-4

US-08-806-203-4
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11150 Santa Monica Boulevard, Suite
                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 3063
TELEPONE: 310-445-1140
INFORMATION: 0445-1140
INFORMATION: 05.045-1010
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 66.7
Matches 2, Conservative
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MOLECULE TYPE: peptide
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STATE: California
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STREET: 11
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Sequence 7, Appli
Sequence 36, Appli
Sequence 19, Appl
Sequence 11, Appl
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                                                                                                                     8, 2003, 09:13:31; Search time 1.85859 Seconds (without alignments) 91.060 Million cell updates/sec
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Sequence 173,
Sequence 37, A
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Sequence 7, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-288-4058-4
US-09-142-078-19
US-09-357-141-19
US-09-357-141-19
US-09-142-080-19
US-09-142-080-19
US-09-486-283C-4-1
US-09-486-283C-4-1
US-08-456-840-38
US-08-456-840-38
US-08-466-138-37
US-08-466-138-38
US-08-466-138-38
US-08-466-138-38
US-08-466-138-38
US-08-466-3438-38
US-08-466-3438-38
US-08-466-3438-38
US-08-475-263-173
US-08-266-4078-38
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-545-151-12
US-08-392-973A-7
US-08-392-973A-8
                                                                                                                                                                                                                                                                                                                        328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents AA:
                                                                                                                                                                                             US-09-498-556C-357
                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                  Copyright
                                                                                                                         December
                                                                                                                                                                                                                                 1 LXRX 4
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Perfect score:
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Gaps

Gaps

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US-08-336-343A-36
Sequence 36, Application US/08336343A
Patent No. 5677144
Patent UN. 5677144
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Frauke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                    Score 9; DB 1; Length 4;
Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 9; DB 1; Length 4; 66.7%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIREAL: ALSO AVOINGE OF LIFE AMERICAS
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REFERENCE/DOCKET NUMBER: 36,742
REFERENCE/DOCKET NUMBER: 36,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF OF OTHER TOWN.
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                 TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7°
2; Conservative
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                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-288-405A-4
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                                                                                                                                                                     amino acid
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US-09-142-078-19
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Sequence 4, Application US/08288405A

Patent No. 5559009

GENERAL INFORMATION:
APPLICANT: Chandy, Kanianthara G.
APPLICANT: Chandy, Grischa
APPLICANT: Gutann, George A.
TITLE OF INVENTION: George A.
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Attn: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
COUNTRY: United States
ZIP: 94111-4187
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG.1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                 ; Sequence 7, Application US/08868452C; Patent No. 6352972; Patent No. 6352972; GENERAL INFORMATION:
; APPLICANT: Marcel E. Nimni; APPLICANT: Enderick L. Hall; APPLICANT: Lingtao Wu APPLICANT: Lingtao Wu APPLICANT: Edwin Shore; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR; TITLE OF INVENTION: USE IN BONE GROWTH; FILE REFERENCE: 1797-211; CURRENT APPLICANTON NUMBER: US/08/868,452C; CURRENT FILING DATE: 1997-06-03; NUMBER OF SEQ ID NOS: 51; SOFTHARE: FRALSEQ for Windows Version 3.0; SEQ ID NO 7; LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 9; DB 4; Length 3;
66.7%; Pred. No. 2.5e+05;
ive 0; Mismatches 1; Indels
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APPLICATION NUMBER: U 08/207,431
FILLING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Malter H.
REGISTRATION NUMBER: 24,190
REPERENCE/DOCKET NUMBER: 4-59844-1/WHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human
US-08-868-452-7
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Gaps

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1; Indels
                          Use of Conantokins for Treating Pain
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SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/533,889
FILING DATE: 22 MAR-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/142,078
FILING DATE: 10-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US97/12652
FILING DATE: 21-JUL-1997
PRIOR APPLICATION NUMBER: US 08/762,377
APPLICATION NUMBER: US 08/762,377
APPLICATION NUMBER: US 08/762,377
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa is gamma-carboxyglutamic acid.
US-09-357-141-19
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ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: D.C.
                                                CURRENT APPLICATION NUMBER: US/09/357,141
CURRENT APPLICATION NUMBER: US/09/357,141
CURRENT FILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1996-02-10
PRIOR PILING DATE: 1996-02-05
PRIOR PILING DATE: 1996-12-06
PRIOR PILING DATE: 1996-11-06
PRIOR PILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Patent No. 6399574
GENERAL INFORMATION:
APPLICANT: McCabe, R. Tyler
APPLICANT: Layer, Li-Ming
APPLICANT: Clivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
TITLE OF INVENTION: Use of Conantokins
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US 08/762,377
06-DEC-1996
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ZIF: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-533-889-19
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Sequence 19, Application US/09142078
Patent No. 6172041
GENERAL INFORMATION:
APPLICANT: McCabe, R. Tyler
APPLICANT: Zhou, Li-Ming
APPLICANT: Layer, Richard T.
TITLE OF INFORMATION: Use of Conantokins
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSER: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
COMPUTER: IRM PC Compatible
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,078
FILING DATE: 10-FEB-1999
PRIOR APPLICATION NUMBER: WO US97/12652
FILING DATE: 21-JUL-1997
PILING DATE: 06-DEC-1996
PRIOR APPLICATION NUMBER: US 08/762,377
FILING DATE: 06-DEC-1996
PRIOR APPLICATION NUMBER: US 08/684,750
FILING DATE: 22-JUL-1996
ATTONERY/AGERT INFORMATION:
NAME: Thean Leff of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Xaa is
gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314-135.A
TELECOMMUNICATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09357141
Patent No. 6277825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olivera, Baldomero M.
McIntosh, J. Michael
McCabe, R. Tyler
Layer, Richard T.
Zhou, Li-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site LOCATION: 4
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Best Local Similarity 66.7
Matches 2; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-357-141-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-142-078-19
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09486283C
; Sequence 4, Application US/09486283C
; Patent No. 6573243
; GENERAL INFORMATION:
    APPLICANT: TYAGAKI, Yasuhiro
; APPLICANT: TYAGAKI, No. 6573243ufumi
APPLICANT: TAKAYANA, Hiroah
; TITLE OF INVENTION: POMPTLID WASP-DERIVED NEUROPEPTIDES
; FILE REFERENCE: 1830/48652
; CURRENT APPLICATION NUMBER: US/09/486,283C
; CURRENT ELING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: DP 9/241699
; PRIOR PILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NOS: 203
; SEQ ID NOS: 203
; SEQ ID NO 4
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-626-923A-12
Sequence 12, Application US/07626923A
Sequence 12, Application US/07626923A
APPLICANT: Yoshimura, Akihiko
APPLICANT: Lodish, Harvey
TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 4; Le
Pred. No. 2.5e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 4; Le
Pred. No. 2.5e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                      LOCATION: 4 OTHER INFORMATION: /note= "Xaa is
                                                                                                                                                                                                                                                                                                            gamma-carboxyglutamic acid"
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                Modified-site
                     TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUIENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                           STRANDEDNESS: «Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pompilid sp.
US-09-486-283C-4
                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LAR 3
                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                    US-09-142-080-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Rothwell, Figg, Brnst & Manbeck, p.c. STREET: 555 Thirteenth Street, N.W., Suite 701-E CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 9; DB 4; Length 4; 66.7%; Pred. No. 2.5e+05; ive 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: /note= "Xaa is OTHER INFORMATION: gamma-carboxyglutamic acid" US-09-533-889-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,080
FILING DATE: 11-May-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US97/12618
FILING DATE: 21-UU-1997
APPLICATION NUMBER: US 08/684,742
FILING DATE: 22-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314-134.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09142080
Patent No. 6515103
GENERAL INFORMATION:
CTUZ, LOURGES J.
Olivera, Baldomero M.
Hillyard, David R.
Hillyard, David R.
Hillyard, David R.
Jimenez, Elsie
Layer, Richard T.
Zhou, Li-Ming
MCCABE, R. Tyler
TITLE OF INVERTION: CONTOCKINS
NUMBER OF SEQUENCES: 71
                                                                                    2314-168.A
FILING DATE: 22-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFREENCE/DOCKET NUMBER: 2314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
                                                                                                                                             TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Conservative
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LXR 3
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US-09-142-080-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 38, Application US/08456840
| Patent No. 559708
| GENERAL INFORMATION:
| APPLICANT: Taddei-Peters, W. C.
| APPLICANT: Taddei-Peters, W. C.
| TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
| NUMBER OF SEQUENCES: 48
| NUMBER OF SEQUENCES: 48
| NUMBER OF SEQUENCES: 48
| STREET: 1330 Piccard Drive | STREET: 1330 Piccard Drive | STREET: Maryland | STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9; DB 1; Length 5; Pred. No. 2.5e+05; 0; Mismatches 1; Indelt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%; Score 9; DB 1; Length 5; 66.7%; Pred. No. 2.5e+05; tive 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,840
FILING DATE: 01-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/266,407
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: US 08/172,461
APPLICATION NUMBER: US 08/172,461
APPLICATION NUMBER: US 08/172,461
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,40; TELECOMUNICATION INFORMATION TELEPHONE: 301-258-5200 TELEFAX: 301-977-0847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7°,
2; Conservative
                                                        TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide
US-08-357-264-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear; MOLECULE TYPE: protein US-08-456-840-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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    : HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/07/626,923A
FILING DATE: 13 December 1990
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: #190-08
TELEPHONE: (617) 861-6240
TELEPAK: (617) 861-6240
TELEPAK: (617) 861-9540
SEQUENCE CHARATICN:
SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: Cushman, Darby & Cushman STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
CONTRY: USA
ZID: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/357,264
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152669
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: US 663897
FILING DATE: 14-MAR-1991
ATTONNEY/ACENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: PNK/5544/202253/DJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5e+05;
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APPLICANT: BURNIE Mr., James P.
APPLICANT: MATTHEWS Ms., Ruth C.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-357-264-5
; Sequence 5, Application US/08357264
; Patent No. 5541077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                         CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5 amino acids
                                                                                                                                                                                             ZIP: 02173
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-07-626-923A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LXR 3
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ADDRESSEE:
STREET: TW
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US-08-406-192-12

Sequence 12, Application US/08406192

Patent No. 5739287

GENERAL INFORMATION:

PAPLICANT: Wilbur, D. Scott

APPLICANT: Prathare, Pradip M

TITLE OF INVENTION: Biotinylated Cobalamins

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christensen, O'Connor, Johnson and Kindness

STREET: 1420 Fifth Avenue, Suite 2800

CITY: Seattle

STRATE: Washington

COUNTRY: US.A.

ZIP: WA 98101-2333

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CUASSIFICATION NUMBER: US/08/406,192

FILING DATE: 16-MAR-1995

CLASSIFICATION NUMBER: US 08/224,831

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Reansoni, George E

REGISTRATION NUMBER: 37,919

REFERENCE/DOCKET NUMBER: RECL18947

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 9; DB 1; Length 5; 66.7%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5
OTHER INFORMATION: /note= "This position is R-NH2."
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 19911107

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURABHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502.20

TELECOMMUNICATION INFORMATION:

TELEFONE: (415) #13-5600

TELEFRA: (415) #13-5600

TELECOMMUNICATION OF SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: AMINO ACID

STRANBEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
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Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-789-184-173
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US-08-406-192-12
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| Patent No. 5688768
| GENERAL INFORMATION:
| APPLICANT: COUGHLIN, SHAUN R.
| APPLICANT: COUGHLIN, ROBERT M.
| TITLE OF INVENTION: RECOMBINANT THROWBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
| TITLE OF INVENTION: RECOMBINANT THROWBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
| TITLE OF INVENTION: RECOMBINANT THROWBIN RECEPTOR AND TITLE OF SEQUENCES: ADDRESSEE: MORRISON & FOERSTER
| STREET: 755 Page Mill Road CITY: Palo Allo STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 1; Length 5; Pred. No. 2.5e+05;
                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BURNIE Mr., James P.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Cushman, Darby & Cushman
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STRATE: 10005-3918

COUNTRY: USA
ZIP: 20005-3918

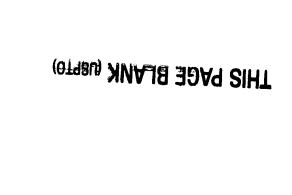
ZIP: 20005-3918

COUNTRY: USA
ZIP: 20005-3918

COUNTRY: BM PC compatible
COMPUTER IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/672,514
FILING DATE: 28-JUN-1996
CLASSIFICATION NUMBER: US 66397
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: US 663897
FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16773
REBERENFE/NOVER-FURGER
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I6773
ER: PNK/5544/202253/DJP
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66.7%; Pred. No. ...
0; Mismatches
                                                          Sequence 5, Application US/08672514 Patent No. 5686248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPERRICE/DOCKET NUMBER: PNK/
TELECOMPUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPK: 6714627 CUSH
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 2, Conservative
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MOLECULE TYPE: peptide
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US-07-789-184-173
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            RESULT 13
US-08-672-514-5
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 8, 2003, 09:20:30 Job time : 2.85859 secs
| TELEPHONE: (206) 682 8100
| TELEFAX: (206) 224 0779
| TELEX: 4938023
| INFORMATION FOR SEQ ID NO: 12:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 5 annino acide
| TYPE: annino acide
| STRANDEDNESS: 8ingle
| TOPOLOGY: linear
| MOLECULE TYPE: peptide
| US-08-406-192-12
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US-09-818-656A-8; Sequence 8, Application US/09818656A; Patent No. US20020142381A1
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LXR 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6, Appli
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                                                                                                                                                                                                                                                                                                               (without alignments)
209.232 Million cell updates/sec
                                                                                                                                                                                                                                                       8, 2003, 09:18:46; Search time 3.55556 Seconds
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(cgnz_6')ptodata/2'/pubpaa/US07_NEW_PUB.ppp:*
(cgnz_6')ptodata/2'/pubpaa/US06_NEW_PUB.ppp:*
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(cgnz_6')ptodata/2'/pubpaa/US10_NEW_PUB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-822-910-5

US-09-852-910-5

US-10-387-467-19

US-10-280-340-674

US-10-280-340-674

US-10-391-399-115

US-10-31-399-116

US-10-028-058-6

US-10-028-058-6

US-10-028-058-6

US-10-028-058-6

US-10-028-058-6

US-10-029-208-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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11
1 LXRX 4
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                December
                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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Sequence 17, Appl
Sequence 9, Appli
Sequence 13, Appl
Sequence 17, Appl
Sequence 1, Appli
Sequence 6, Appli
                                                                                                                                           Sequence 693, App
Sequence 693, App
Sequence 80, Appl
Sequence 4, Appli
Sequence 1, Appli
Sequence 37, Appli
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Sequence
Sequence
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US-10-006-557-7

US-02-486-734A-17

US-09-486-734A-17

US-09-70-102A-17

US-09-70-102A-17

US-09-500-700-73

US-09-500-700-73

US-09-500-700-73

US-10-308-89

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-6168-6

US-10-31-31-88-80

US-10-24-709-4

US-09-779-233-31

US-09-779-233-42

US-09-779-233-42

US-09-779-233-42

US-09-779-233-43

US-09-779-233-44

US-09-779-233-43

US-09-989-789-125

US-09-989-789-125
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Sequence 2, Application US/09248158
Patent No. US20020015678A1
GENERAL INFORMATION
APPLICANT: Yuan, Zhengyu
APPLICANT: Chen, Zhong-Xiao
ITILE OF INVENTION: Direct Adsorption Scintillation Assay
TITLE OF INVENTION: For Measuring Enzyme Activity and Assaying Biochemical
ITILE OF INVENTION: Processes
FILE REFERENCE: 342312000600
CURRENT APPLICATION NUMBER: US/09/248,158
CURRENT FILING DATE: 1999-02-09
PRIOR FILING DATE: 1998-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 4; 6.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 9;
Pred. No. 6.1e+
0; Mismatches
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic peptide US-09-248-158-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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Gaps

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0
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                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 9; DB 11; Length 4; 66.7%; Pred. No. 6.1e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                    FEATURE:
NAMEKEY: misc_feature
LOCATION: (1)...(4)
LOCATER INFRMATION: G alpha t library linker sequence
US-09-852-910-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314-256.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/142,080 FILING DATE: 15-MAY-2000 APPLICATION NUMBER: WO US97/12618 FILING DATE: 21-UL-1997 APPLICATION NUMBER: US 08/684,742 FILING DATE: 22-ULL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/357,467
FILING DATE: 04-Feb-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-357-467-19
Sequence 19, Application US/10357467
Publication No. US20030194729A1
CENERAL INFORMATION:
APPLICANT: Abogadie, Fe C.
CTUZ, LOUZGES J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cruz, Lourdes J.
Olivera, Baldomero M.
Walker, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colledge, Clärk
Hillyard, David R.
Jimenez, Elsie
TITLE OF INVENTION: Conantokins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4 amino acids
SOFTWARE: Patentin version 3.0
SEQ ID NO 155
LENGTH: 4
                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 66...
المالية 25 Conservative 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LTR 4
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18.09-862-910-155

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APPLICANT: Hamm, Heidi
APPLICANT: Glichrist, Annette
APPLICANT: Glichrist, Annette
TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
FILE REPERENCE: 2661-101
CURRENT APPLICATION NUMBER: US/09/852,910
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US 60/275,472
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEC ID NOS: 271
SOFTWARE: Patentin version 3.0
                           APPLICANT: GONG, Fangcheng et al.

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOL191

CURRENT APPLICATION NUMBER: US/09/818,656A

CURRENT FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 103

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 9; DB 10; Length 4; 66.7%; Pred. No. 6.1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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; OTHER INFORMATION: PAR-23
US-09-852-910-5
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LTR 4
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US-09-852-910-5
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51158-20050.00
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Publication No. US20030199470A1

SEQUENCE LINCORANTION:

APPLICANT: FARIS, MARY

APPLICANT: HUBERT, RENE

APPLICANT: HUBERT, AND

TITLE OF INVENTION: OTHER CANCERS

TITLE OF INVENTION: UMBER: US/10/277,292

CURRENT APPLICATION NUMBER: US/09/935,430

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 700

SOFTWARE: PATENT NOS: 700

SSOFTWARE: PATENT NO 674

LEMENT ALTHER PATENT NO 674
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                1; Indels
                                                                                                                                             Score 9; DB 12; Length 4;
Pred. No. 6.1e+05;
0; Mismatches 1; Indels
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                              "Xaa is
LOCATION: 4
OTHER INFORMATION: /note= "Xaa
gamma-carboxyglutamic acid"
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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                                                                                                                                           81.8%;
66.7%;
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APPLICANT: HUBBET, RENB
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LENIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOVITZ, AYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                    Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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GENERAL INFORMATION
                                                                                                                                                                                                                                              1 LXR 3
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US-10-277-292-674
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                                                                                                US-10-357-467-19
                                                                                                                                                Query Match
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PRDICATION NO. US2000219806A1

GENERAL INPORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glouksmann, Maria Alexanndra
APPLICANT: Glouksmann, Maria Alexanndra
APPLICANT: Curtis, Rory J. J.
APPLICANT: Curtis, Rory J. J.
APPLICANT: Glouksmann, Maria Alexanndra
APPLICANT: Glouksmann, Maria Alexanndra
APPLICANT: Siloe-Santiago, Immaculada
ITILE OF INVENTION: NOVEL 1867, 15603, 69318, 12303, 48000,
ITILE OF INVENTION: NOVEL 1867, 1533, 38554, 57301, 58324, 55065, 52991, 59914, 59921
ITILE OF INVENTION: NOVEL 1867, 1571 MOLECULES AND USES THEREFOR
ITILE OF INVENTION: AND 13751 MOLECULES AND USES THEREFOR
ITILE OF INVENTION: AND 13751 MOLECULES AND USES THEREFOR
ITILE OF INVENTION: AND 13751 MOLECULES AND USES THEREFOR
CURRENT FILING DATE: 2003-03-18
PRIOR FILING DATE: 2004-02-2
PRIOR PELLORATION NUMBER: US 99/583,373
PRIOR PELLORATION NUMBER: US 99/583,373
PRIOR PELLORATION NUMBER: US 10/309,804
PRIOR PELLORATION NUMBER: US 10/309,804
PRIOR FILING DATE: 2002-12-04
PRIOR PELLORATION NUMBER: US 10/309,804
PRIOR FILING DATE: 2002-13-08
PRIOR FILING DATE: 2002-13-08
PRIOR FILING DATE: 2002-13-08
PRIOR FILING DATE: 2002-13-08
PRIOR FILING DATE: 2003-03-08
PRIOR PELLORATION NUMBER: US 60/195,734
PRIOR PELLORATION NUMBER: 
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6.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 9; DB 1
66.7%; Pred. No. 6.1e
tive 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/280,340
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US/09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR PLILNG DATE: 2000-08-22
PRIOR PLILNG DATE: 2000-08-22
PRIOR PLILNG DATE: 2001-08-22
PRIOR PLILNG DATE: 2001-08-22
PRIOR PLILNG DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
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Publication No. US20030219806A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 66.7
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APPLICANT: Hudson, B.
TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer FILE REPERENCE: WBHB 01-1017
CURRENT APPLICATION NUMBER: US/10/206,699
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/308,523
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-32
PRIOR FILING DATE: 2002-03-31
PRIOR FILING DATE: 2002-03-31
PRIOR FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: swiss/p36507/MPK2 Human US-10-028-075B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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APPLICANT: Benner, Robert
TITLE OF INVENTION: Oligopeptide treatment of anthrax FILE REFERENCE: 2183-52220S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 9; DB 15; I
66.7%; Pred. No. 6.1e+05;
iive 0; Mismatches 1;
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; Sequence 6, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisax A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REPRENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT APPLICATION NUMBER: EP 01203748.7
; PRIOR APPLICATION NUMBER: EP 01203748.7
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 6
; LENGTH: 4
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ORGANISM: Artificial Sequence
FEATURE:
                              APPLICANT: Sundaramoorthy, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66...
2, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-206-699-295
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US-10-028-075B-6
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APPLICANT: Gluckemann, Maria Alexanndra
APPLICANT: Guctis, Rory A. J.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Katherine M.
APPLICANT: Silos-Santiago, Inmaculada
ITILE OF INVENTION NOVEL 18603, 48031, 88354, 57301, 88334, 55083, 52991, 59914, 59921
ITILE OF INVENTION NOVEL 18603, 13751 MOLECULES AND USES THEREFOR PLEASE METEROR MAD 33751 MOLECULES AND USES THEREFOR CURRENT APPLICATION NUMBER: US 09/789, 481
PRIOR PELING DATE: 2000-08-08
PRIOR PELING DATE: 2000-08-08
PRIOR PELING DATE: 2000-08-18
PRIOR PELING DATE: 2000-08-18
PRIOR PELING DATE: 2000-08-19
PRIOR PLING DATE: 2000-08-19
PRIOR PLING DATE: 2000-08-19
PRIOR PLING DATE: 2000-08-19
PRIOR PLING DATE: 2000-12-49
PRIOR PLING DATE: 2000-12-49
PRIOR PLING DATE: 2001-12-49
PRIOR PLING DATE: 2001-12-40
PRIOR PRIOR DATE: 2001-12-40
PRIOR PLING DATE: 2001-03-12
PRIOR PLING DATE: 2001-03-12
PRIOR PLING DATE: 2001-03-12
PRIOR PLING DATE: 2001-12-40
PRIOR PLING DATE: 2001-12-40
PRIOR PLING DATE: 2001-03-12
PRIOR PLING DATE: 2001-03-13
PRIOR PLING
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                                                                                 Score 9; DB 12; Length 4;
Pred. No. 6.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: N-glycosylation site US-10-391-399-116
, OTHER INFORMATION: N-glycosylation site US-10-391-399-115
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US-10-206-699-295
'Sequence 295, Application US/10206699
'Phylication No. US20030100510A1
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 116, Application US/10391399; Publication No. US20030219806A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                           81.8%;
66.7%;
                                                                                        Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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US-10-391-399-116
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; Dublication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: NOZZELLE, James
; APPLICANT: NOZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; CURRENT APPLICATION NUMBER: 60/334,434
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR PILING DATE: 2001-11-30
; NUMBER OF SEC ID NOS: 58
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 36
; LENATUS. 5
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                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASSESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,123
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-NO. US20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
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Pred. No. 6.1e+05
0; Mismatches
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Pred. No. 6.1e+
0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                               FILING DATE: 04-Apr-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415). 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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66.7%;
                                                   San Francisco
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Best Local Similarity 66.7
Matches 2; Conservative
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US-10-302-817A-36
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TITLE OF INVENTION: APFINITY SELECTED SIGNATURE PEPTIDES FOR PROTEIN IDENTIFICATION JUNE PRICE REPERINCE: 290.0001 0103
CURRENT APPLICATION NUMBER: US/10/244,709
CURRENT APPLICATION NUMBER: 60/203,227
PRIOR PELING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/203,184
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Pred. No. 6.1e+05;
0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/029,206A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108, Application US/10407123 Publication No. US20030181381A1 GENERAL INFORMATION: APPLICANT: Himmelspach, Michele
                  CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/821,380
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 175
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/208,372
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERBION 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10244709
Publication No. US20030129769A1
GENERAL INFORMATION:
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Fisch, Andreas
Eibl, Johann
                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-407-123-108
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1 LXR 3 | | | 1 LSR 3

Search completed: December 8, 2003, 09:34:04 Job time : 4.55556 secs

G protein coupled
G protein coupled
Novel human transp
Accessory moiety d

Ovine growth hormo Ovine growth hormo Ovine growth hormo Human apolipoprote

Cyclic pentapeptid Cyclic pentapeptid Cyclic pentapeptid Subtilisin N62D/G1 Mammalian heemoglo AAV VP3 derived pe Tryptic peptide #1

Chymotryptic pepti MASP substrate #3. Human rBPI protein Targetting peptide PSA antibody prepa PSA antibody prepa

Spinacia oleracea Proteome analysis Phytase derived pe Ovine growth hormo

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Ovine growth hormo dsRNA-dependent ki 3-methylcholanthre

Hybridoma ATCC HB-

Complement antagon Mammalian haemoglo

Peptide immunoreac Pancreatic polypep

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Soybean diverged d C-terminal sequenc PSA antibody prepa PSA antibody prepa

Score

Result Š. 26459786

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Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Database

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Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth.
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                                                                                                                                                                                                 AAW37317
AAY51458
AAE11109
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AAE05461
AAE26308
                                                                                                                                                                                                                                                                                                                                                   ABP55342
ABP75051
AAR46808
AAR50141
AAR50142
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AAW00251
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   98WO-US11189
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NIMNI M E.
SHORS E C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HALL/) HALL F L.
(HANB/) HAN B.
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(SHOR/)
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Peptide comprising
Conantokin peptide
Conantokin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequenc
BoNT/A N-glycosyla
                                                                                                   ; Search time 5.45455 Seconds (without alignments)
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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            5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     1107863 seqs, 158726573 residues
            GenCore version (c) 1993 - 2003
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                                                                                                   2003, 09:13:30
                                                                       sw model
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Maximum Match 100%
Listing first 45 summaries
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AAW49964
AAG79019
AAE24457
AAE20561
AAE14417
AAM51953
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Gapop 10.0 , Gapext 0.5
                                                                     - protein search, using
                                                                                                                                                              US-09-498-556C-357
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Maximum DB seq length: 200000000
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Match Length
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RESULT 3
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                                                                                                                                                         The present peptide represents a proteinase site used in the creation of the bone morphogenetic fusion proteins of the invention. The bone morphogenetic fusion protein may contain some or all of the following elements: a purification tag a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment. The fusion proteins of the invention also includes proteins that have transforming growth factor beta active fragments instead of bone morphogenetic protein active fragments. The bone morphogenetic fusion proteins can be used for enhancing wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New conantokin peptide(s) - useful for e.g. treating neurologic or psychiatric disorders, or the management of pain
                                    New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conantokin; predatory cone snail; treatment; neurologic disorder; psychiatric disorder; anticonvulsant; neuroprotective; analgesic. HIV infection; ophthalmic indication; memory; learning defect;
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Rivier JE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 20; Length 3;
Pred. No. 9.2e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "gamma-carboxyglutamic acid"
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Layer RT, McCabe RT, Olivera BM, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW48182 standard; peptide; 4 AA.
                                                                                                                    Claim 8; Page 34; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conantokin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
66.7%;
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(UTAH ) UNIV UTAH RES FOUND
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Best Local Similarity 66.7%,
Best Active
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Zhou L;
WPI; 1999-059875/05.
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                                                                                                                                                                                                                                                                                                                                                                                          3 AA;
                                                                                                                                                                                                                                                                                                                                                  bone growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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The present sequence is a conantokin peptide derivative, which can be used to treat neurologic and psychiatric disorders, e.g. as an anticonvulsant, neuroprotective or analysesic agent. Neurologic and psychiatric disorders include epilepsy, convulsions, neurotoxic constructions of hypoxia, anoxia or ischaemia, microflation stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyria or hypoglycaemic events), curvodegeneration (associated with Alzheimer's disease, semile dementia, Amyotrophic Lateral Sclerosis, Multiple Sclerosis, Paxkinson's disease, Huntington's disease, Down's Syndrome, carakoff's disease, schizophrenia, AlDS dementia, multi-infarct dementia, Binswanger dementia and neuronal damage associated with curcontrolled seizures), chemical toxicity (such as addiction, and morphine, opiate, opioid and barbiturate tolerance), pain (acute, offonio: migraine), anxiety, major depression, manic-depressive, cillness, obsessive-compulsive disorder, unipolar depression, dysthymia and seasonal effective disorder, unipolar depression, dysthymia and seasonal effective disorder, unipolar depression, dysthymia captide can also be used to treat HIV infection, ophthalmic peptide can also be used to treat HIV infection, ophthalmic indication and memory, learning or cognitive defects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 9.2e+05;
0; Mismatches 1;
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66.7%;
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Best Local S
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Matches
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be used to treat neurologic and psychiatric disorders, e.g. as anticonvulsant, neurologic and psychiatric disorders, e.g. as anticonvulsant, neuroprotective or analgesic agent. Neurologic and psychiatric disorders include epilepsy, convulsions, neurotoxic injury (associated with conditions of hypoxia, anoxia or ischaemia, which typically follow stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events), centrodegeneration (associated with Alzheimer's disease, senile demential, Amyotrophic Lateral Sclerosis, Multipple Sclerosis, Parkinson's disease, Huntington's disease, Down's Syndrome, Corsakoff's disease, Schizophrenia, AIDS dementia, multi-infarct dementia, Binmanger dementia and neuronal damage associated with uncontrolled seizures), chemical toxicity (such as addiction, and morphine, opiate, opioid and barbiturate tolerance), pain (acute, offonic, migraine), anxiety, major depression, manic-depressive illness, obsessive-compulsive disorder, unipolar depression, dysthymia and seasonal effective disorder, unipolar depression, dysthymia and seasonal effective disorder, unipolar disorder, innipolar disorder), and seasonal effective disorder, unipolar disorder, innipolar disorder), and seasonal effective disorder, unipolar disorder), and seasonal effective disorder, and escapanic disorder and environment disorder), and environment disorder) and environment disorder).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sleep disorder, muscle relaxation and urinary incontinence. The peptide can also be used to treat HIV infection, ophthalmic indication and memory, learning or cognitive defects.
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                                                                present sequence is a conantokin peptide derivative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "gamma-carboxyglutamic acid"
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                     Claim 27; Page 69; 122pp; English.
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96US-0762377.
97WO-US12652.
99US-0142076.
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Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG79019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
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of cone snalls. They are used for the treatment of disorders in which excitation of marve calls by excitatory amino acids or agonist of N-methyl-D-aspartate (NMDA) receptor. The conancokin peptides are used for the treatment of disorders such as pain; neurologic or psychiatric disorders such as pain; neutrologic or psychiatric disorders such treatment of hypoxia, anoxia or ischemia; for treating neurodegeneration; for breating chemical toxicity such as addiction, drug craving, alcohol abuse, morphine, opioid and barbiturate tolerance; for treating psychiatric disorders such as anxiety, major depression, manic-depression illness, obsessive compulsive disorder, schizophrania or mood disorder; for treating odditional neurological disorders e.g. dystonia, sleep disorder; muscle relaxation and urinary incontinence; for memory/cognition enhancement; for treating HIV
                                                                                                                                                                                                          AAG79012-43 and AAG790054-56 represent domains of conantokin peptides. Conantokins differ from conotoxins, in that they contain gamma-carboxyglutamic acid. The conantokins are derived from the venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                             Use of conantokin peptide or its derivatives or a conantokin peptide chimera for treating disorders e.g. migraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spaemodic dysphonia, laryngeal dystonia, muscular tension, asthma, neuralgia, autonomic nervous system disorder, sweating, salivation, headache, neuropathy, botulinum toxin serotype A, BoNT/A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurotoxin; biological persistence; blepharospasm; pain; therapy; neuromuscular disorder; cervical dystonia; oromandibular dystonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Leus.
3. 9.2e+05; Indels
                                                                Zhou L;
                                                                Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9; DB 22
Pred. No. 9.2e+
0; Mismatches
                                                                Mccabe RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                             Claim 9; Column 80; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE24457 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BoNT/A N-glycosylation site #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spanoyannis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2001; 2001WO-US44030.
                 (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALLR ) ALLERGAN SALES INC
                                                                Olivera BM, McIntosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum
                              (COGN-) COGNETIX INC
                                                                                           WPI; 2001-601377/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200240506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steward LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE24457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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Sioma CS,
                                                                                                                  256-259).
                                                                                                                                                                                                                                                                                                                   AAE14417;
                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RIGG/)
(SIOM/)
(WANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PURD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZHAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (לננונ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENG/
                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                 AAE14417
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                                                                                                  The invention related to modified neurotoxins especially Clostridial botulinum toxins with altered biological persistence. These toxins comprise a structural modification which is effective to alter the biological persistence. Modified neurotoxins of the invention are used for treating biological disorders which include neuromuscular disorder e.g. strabismus, blepharospasm, spasmodic torticollis (cervical dystonia), oromandibular dystonia and spasmodic dysphonia (laryngaal dystonia), autonomic nervous system disorders e.g. excessive salivation and sweating, asthma etc. and pain e.g. headache, muscular tension, neuralgia and neuropathy. The present sequence is botulinum toxin services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-
                    Modified neurotoxin especially Clostridial toxins, useful for treating neuromuscular and autonomic nervous system disorder and pain, comprises structural modification to alter biological persistence of neurotoxin
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly- and unsaturated fatty acids and in increasing the unsaturation levels in cellular lipids -
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean diverged delta-9 fatty acid desaturase peptide #7.
                                                                                                                                                                                                                                                                               81.8%; Score 9; DB 23; Length 4; 66.7%; Pred. No. 9.2e+05;
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinney AJ,
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                 Disclosure; Page 19; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 48; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              AAE20561 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-2001; 2001WO-US26246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2000; 2000US-226996P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                        2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269353/31.
 WPI; 2002-479904/51.
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                          4 AA;
                                                                                                                                                                                                                                                                                                                              1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200216565-A2
                                                                                                                                                                                                                                   botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Booth JR,
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE20561;
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mnore, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides and be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is soybean diverged delta-9 fatty acid desaturase peptide (residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riggs LD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein quantification; protein identification; signature peptide; mass spectrometric analysis; proteolytic peptide; affinity ligand; arginine; isobaric peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analyzing differences in protein content in protein samples, identifying protein(s) in a sample or multiple proteins in a complex mixture, by employing mass spectrometric analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ji J,
                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 4;
9.2e+05;
ches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-terminal sequence of an arginine-containing peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G'eng M,
                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 23
Pred. No. 9.2e4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dormady SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 73; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE14417 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chakraborty AB, ang S, Zhang X;
                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2001; 2001WO-US14418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2000; 2000US-208184P. 31-MAY-2000; 2000US-208372P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGNIER F E.
CHAKRABORTY A B.
DORMADY S J.
G'ENG M.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PURDUE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-089810/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIGGS L D.
SIOMA C S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WANG S.
ZHANG X.
                                                                                                                                                                                                                                                                                                                                  4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200186306-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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us-09-498-556c-357.rag

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of proteolytic peptide fragments. The method comprises

Cragmenting at least a first protein sample and a second protein

Establishmenting at least a first protein sample and a second protein

ample to produce a first peptide pool and a second peptide pool;

least one of the pools so as to permit resolution of the peptides in at

least one of the pools so as to permit resolution of the cherwise

identical peptides in the first and second peptide pools by mass

analysis; contacting peptides from at least a portion of both of the

peptide pools with a capture moiety to yield affinity-selected peptides

comprising an affinity ligand, where the capture moiety selects for the

affinity ligand; and analysing the affinity-selected peptides by mass

spectrometry to determine one or more differences between the first and

second samples. The method of the invention is useful for identifying one

or more proteins in the sample, and is typically useful for identifying

multiple proteins in a single complex mixture. The method is also useful

cor quantifying proteins in a sample complex mixture. The advantages

of the novel method are that it is easier to separate peptides than

priving the analysis returners of the protein does not have to be maintained

proteins; native structure of the protein does not have to be maintained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification of a protein in a complex sample without purifying the protein or obtaining its composite peptide signature. The present sequence is C-terminal fragment of a differentially acetylated arginine-containing peptide which is used to generate fragment ions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an antibody specific for (-5,-6 and -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)
    employing mass spectrometric analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate-specific antigen; prostatic carcinoma; pro-kallikrein 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody comprising specificity for some truncated forms of pro-prostate specific antigen, useful in immunoassays for differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          putative proteins suggested from DNA database can be recognised by using a signature peptide probe. The present method permits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                     during the analysis; structural variants do not interfere; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 9; DB 23; Length 4; 66.7%; Pred. No. 9.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSA antibody preparation immunogen peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 11; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              distinguishing isobaric peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM51953 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of prostatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000; 2000DE-1032040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2000; 2000DE-1025387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; antibody; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-042633/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE10032040-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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or shorter forms of the protein. The antibody can be used to diagnose prostatic carcinome and to detect human pro-kallikrein 2. The present sequence is a peptide which forms part of a peptide-containing immunogen described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an antibody specific for (-5,-6 and -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4) or shorter forms of the protein. The antibody can be used to diagnose prostatic carcinoma and to detect human pro-kallikrein 2. The present sequence is a peptide which forms part of a peptide-containing immunogen described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody comprising specificity for some truncated forms of pro-prostate specific antigen, useful in immunoassays for differential diagnosis of prostatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                     PSA; prostate-specific antigen; prostatic carcinoma; pro-kallikrein 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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3.2e+05;
1.a | 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 23; Length 4;
Pred. No. 9.2e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       PSA antibody preparation immunogen peptide #9.
                                                                                                                           0; Mismatches
                                                                                                 Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 11; 16pp; German.
                                                                                                                                                                                                                                                    AAM51957 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ36682 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) ROCHE DIAGNOSTICS GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
                                                                                              81.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000; 2000DE-1025387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2000; 2000DE-1032040
                                                                                                                                                                                                                                                                                                                                                                                human; antibody; immunogen.
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                           2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                       4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA;
                                                                                                                                                       1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         DE10032040-A1.
                                                                                                                                                                                                                                                                                                            01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2001.
                                                                                                                                                                                                                                                                                AAM51957;
                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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ABJ3682
ID ABJ36
XX
AC ABJ36
                                                                                                                           Matches
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  8X333X8
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antibacterial; analgesic; antiallergic; antiasthmatic; antiinflammatory; osteopathic; neuroprotective; anxiolytic; anorectic; lead compound; grotein coupled receptor signaling inhibitor; GPCR; library; high throughput screening assay; stroke; myocardial infarction; restenosis; atherosclerosis; hypotension; cancer; infection; asthma; septic shock; pain; allergic disorder; inflammatory bowel disease; osteoporosis; obsity; psychotic; neurological disorder; anxiety;
                                                                                                                                                          Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying G protein coupled receptor (GPCR) signaling inhibitors, useful in screening drugs for treating stroke, cancers or pain, by identifying compounds that block GPCR mediated signaling with high
                                                                                                     G protein coupled receptor related peptide SEQ ID No 155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 178; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                      schizophrenia; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2001; 2001US-275472P.
11-MAY-2001; 2001US-0852910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2002; 2002WO-US07561.
                                                    01-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity and specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilchrist A, Hamm HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CUEB-) CUE BIOTECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-247841/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200272778-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-2002
ABJ36806;
The invention relates to a novel method for identifying a G protein coupled receptor (GPCR) signaling inhibitor. The novel method comprises selecting or identifying a member of a library of peptides and/or candidate compounds, having binding to a GPCR of higher affinity than that of the native peptide. The peptide library is based on a native GPCR binding peptide. The method is useful for identifying inhibitors of a G protein coupled receptor (GPCR) signaling. The method is particularly useful for identifying drugs that antagonise the binding between a GPCR and its extracellular ligand(s). The method is especially useful in modern high throughput screening assays for identifying potent lead compounds. The compounds, peptides or inhibitors identified by the method are useful for preventing, andiorating or treating diseases in which GPCR signaling is a causative factor or in which a specific class of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein is relevant, e.g. stroke, myocardial infarction, restenosis, atherosclerosis, hypotension, cancers, infections, septic shock, pain, allergic disorders, asthma, inflammatory bowel disease, osteoporosis, obesity, or psychotic and neurological disorders (e.g. anxiety, schizophrenia or Alzheimer's disease). This sequence represents a peptide relating to the G protein coupled receptors of the invention.
                                                                                                Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic; antibacterial; analgesic; antiallergic; antiasthmatic; antinflammatory; osteopethic; neuroprotective; anxiolytic; ancettic; lead compound; g protein coupled receptor signaling inhibitor; GPCR; library; high throughput screening assay; stroke; myocardial infarction; restenosis; atherosclerosis; hypotension; cancer; infection; asthma; septic shock; pain; allergic disorder; inflammatory bowel disease; obteoporosis; obesity; psychotic; neurological disorder; anxiety; schizophrenia; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying G protein coupled receptor (GPCR) signaling inhibitors, useful in screening drugs for treating stroke, cancers or pain, by identifying compounds that block GPCR mediated signaling with high affinity and specificity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 9; DB 24; Length 4; 66.7%; Pred. No. 9.2e+05; ive 0; Mismatches 1; Indels
                                                    G protein coupled receptor related peptide SEQ ID No 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 12; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2001; 2001US-275472P.
11-MAY-2001; 2001US-0852910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2002; 2002WO-US07561
01-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilchrist A, Hamm HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-247841/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CUEB-) CUE BIOTECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200272778-A2.
                                                                                                                                                                                                                                                                                                                                                                      Mammalia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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The invention relates to a novel method for identifying a G protein coupled receptor (GPCR) signaling inhibitor. The novel method comprises selecting or identifying a member of a library of peptides and/or candidate compounds, having binding to a GPCR of higher affinity than that of the native peptide. The peptide library is based on a native GPCR binding peptide. The method is useful for identifying inhibitors of a G protein coupled receptor (GPCR) signaling. The method is particularly useful for identifying daugs that antagonise the binding between a GPCR and its extracellular ligand(s). The method is especially useful in modern high throughput screening assays for identifying potent lead compounds. The compounds peptides or inhibitors identified by the method are useful for preventing, ameliorating or treating diseases in which are useful for preventing, ameliorating or treating diseases in which compounds a subjactive factor or in which a specific class of G protein is relevant, e.g. stroke, mycozadial infarction, restenosis, atherosclerosis, hypotension, cancers, infections, septic shock, pain, atherosclerosis, hypotension, cancers, infections, septic shock, pain, cobesity, or psychotic and neurological disorders (e.g. anxiety, cobesity, or psychotic and neurological disorders (e.g. anxiety, callaring to the G protein coupled receptors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 9; DB 24; Length 4; 66.7%; Pred. No. 9.2e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LXR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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ABU13761
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1; Indels

Local Similarity 66.7 nes 2; Conservative

Best Loc Matches

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1 LXR 3

ABJ36806 standard; Peptide; 4 AA.

RESULT 11 ABJ36806 ID ABJ3

ABU13761 standard; Peptide; 4 AA

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Novel human transporter protein, related to gamma-aminobutyric acid neurotransmitter transporter subfamily useful as model for developing human therapeutic targets and serves as target for human therapeutics
                                                       Human; gamma-aminobutyric acid; GABA; neurotransmitter transporte
transgenic animal; ribozyme design; drug screening; gene therapy.
                                         Novel human transporter protein related peptide #4.
                                                                                                                                                                                      Di Francesco V, Beasley EM;
                                                                                                                        28-MAR-2001; 2001US-0818656
                                                                                                                                      28-MAR-2001; 2001US-0818656
                           (first entry)
                                                                                                                                                         KETCHUM K A.
DI FRANCESCO V.
                                                                                                                                                                                       Ketchum KA,
                                                                                                                                                                         BEASLEY E M.
                                                                                                                                                                                                     WPI; 2003-102517/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
                                                                                           JS2002142381-A1
                                                                                                                                                    GONG F.
                                                                              Homo sapiens
                            25-FEB-2003
                                                                                                        03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                       Gong F,
                                                                                                                                                            (KETC/)
(DFRA/)
                                                                                                                                                   (CONG/)
                                                                                                                                                                         (BEAS/)
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Fritzberg AR;

Abrams PG, Nichols EJ,

Morgan AC,

Anderson DC,

CORP.

(NEOR-) NEORX

WPI; 1990-085154/12.

89EP-0250014. 88US-0232337

14-AUG-1989; 15-AUG-1988;

21-MAR-1990. EP359347-A. Synthetic.

Accessory moiety; transferrin receptor; tumour therapy. Accessory moiety derived from transferrin receptor.

AAR03446 standard; protein; 5 AA.

RESULT 13 AAR03446

2 LTR

(first entry)

02-AUG-1990

AAR03446;

GABA; neurotransmitter transporter;

Covalently linked complex for tumour treatment - comprises treating with protein, cytotoxic agent and enhancing moiety.

Claim 13; Page 22; 23pp; English.

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in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This is the amino acid sequence of a polypeptide related to the novel human aminobutyric acid (GABA) transporter related protein.
                                                                                                                                                                                                                                                                                                                                                                         (GABA) transporter related protein
Disclosure, Page 45; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                      attached to the C-terminus of a manchering modery which in turn is linked to a targeting protein and a cytotoxic agent. When the anchoring peptide intercalates into the target cell plasma membrane the accessory moiety is translocated across the membrane and protrudes into the cytoplasm. It can then be phosphorylated by cellular kinases at neutral pH. This irreversibly anchors the complex to the membrane and may enhance the translocation into the cytoplasm. The complex is useful for treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                              The sequence is one of several possible accessory moieties which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of portion of wild-type murine erythropoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9; DB 11; Length 5;
Pred. No. 9.2e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR48999 standard; Protein; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erythropoietin receptor; EPO; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA;
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Query Match
81.8%; Score 9; DB 24; Length 4;
Best Local Similarity 66.7%; Pred. No. 9.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels

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Search completed: December 8, 2003, 09:16:40
                                                                                                                                                                                                                                                                          Job time : 6.45455 secs
                                                                                                                                                         5 AA;
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                                                                                                                                                                                                                                    2 LSR
                                                                                                                                                          Sequence
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Best Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                           nEPOR is wild-type EPOR. CEPOR is a constitutive EPOR. It contains a point mutaion (a transition from C to T at nucleotide 484) which causes one substitution (Arg to Cys) in the exoplasmic domain of EPOR at codon 129 of the predicted N-terminus. The ARg to Cys point mutation in CEPOR is sufficient to induce factor-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine, ovine, porcine, growth hormone, bGH; oGH; pGH; antigen, growth hormone activity; potentiate, enhance, increase.
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                    Mutant erythropoietin (EPO) receptor gene - hypersensitive to EPO, useful in assay for identifying compounds, mimicking EPO
                                                                                                                                                                                                                                                                                                                                   81.8%; Score 9; DB 15; Length 5; 66.7%; Pred. No. 9.2e+05; ive 0; Mismatches 1; Indels
                                                                                                                  (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                    /note= "Cys in cEPOR"
                                                                                                                                       Lodish H, Longmore GD, Yoshimura A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovine growth hormone residues 92-96.
Location/Qualifiers
                                                                                                                                                                                                                           Disclosure; Fig 1C; 13pp; English.
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(HANN-) HANNAH RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR50135 standard; peptide; 5 AA.
                                                                             90US-0626923.
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93GB-0016508.
                                                                                                90US-0626923
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(first entry)
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Best Local Similarity 66.77
                                                                                                                                                         WPI; 1994-082328/10.
                                                                                                                                                                   N-PSDB; AAR48999
                                                                                                                                                                                                                                                                                                                5 AA;
 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                        1 LXR 3
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                                                                             13-DEC-1990;
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09-AUG-1993;
                                                                                               13-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9405697-A1
                                                         08-MAR-1994.
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23-SEP-1994
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                                       US5292654-A
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Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus.
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                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                             growth.
                                                                                                                                                                                                          action
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                                                                                                                   New antigenic molecules derived from growth hormone - and derived antibodies, used to stimulate the activity of growth hormone
                                                                                                                                                                                                                                                                  This peptide corresponds to residues 92-96 of bovine, ovine and porcine growth hormone. The peptide is rendered antigenic and is then capable of stimulating the production of antibodies which, when in the appropriate formulation, potentiate the effect of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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Pred. No. 9.2e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              growth hormone. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                Claim 4; Page 7; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity 66.7%;
2; Conservative
Beattie J, Holder AT;
                                                              WPI; 1994-101122/12.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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sw model
3
using
search,
protein
1
OM protein
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December 8, 2003, 09:13:30 ; Search time 4.20202 Seconds (without alignments) 245.646 Million cell updates/sec Run on:

US-09-498-556C-357

1 LXRX 4 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:* Database :

pp_cramelle:*
sp_phage:*
sp_phage:*
sp_rodent:*
sp_vrons:*
sp_vrtebrate:*
sp_unclassified:*
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sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Query				
	Match	Match Length DB	DB	ID	Description
2 8 4 8 3 2 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	81.8	8	4	016468	O16468 homo sapien
11 10 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	81.8	80	8	09T4Y2	09t4v2 asterina pe
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11. 110087051 11009999999	81.8	6	œ	Q9T688	O9t688 gecko gecko
11 10 10 10 10 10 10 10 10 10 10 10 10 1	81.8	0	æ	Q94VH4	094vh4 varanus gla
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8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	81.8	σ	8	Q94VI8	094vi8 varanus ere
10 9 9 9 9	81.8	0	œ	094VC6	Varanus
110000	81.8	σ,	80	094VE1	O94vel varanus mer
11 6	81.8	σ	12	Q91BM8	
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77	81.8	10	80	Q958K9	0958k9 rana bovlii
13 9	81.8	10	80	Q9TG86	09tq86 diploglossu
14 9	81.8	10	8	094V97	094v97 varanus spe
15 9	81.8	10	8	Q94VD5	094vd5 varanus oli
16 9	81.8	10	œ	094VC9	094vc9 varanus pan

Q94vfO varanus kin Q9tg47 ophisaurus P92771 xenosaurus Q94v65 varanus var Q9tg32 ophisaurus				078121 oreochromis 077904 oreochromis 077903 oreochromis 077903 oreochromis 094v94 varanus sto 099621 calotes nig 099408 varanus gou 099365 calotes emm
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ALIGNMENTS

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	PRELIMINARY;		(TrEMBLrel. 01,	(TrEMBLrel. 10,	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	DNA for cosmid cC13-1134 PCR primer 1 (Fragment).	B (Human).	Metazoa; Chordata	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	9096;		OM N.A.	MEDLINE=96435920; PubMed=8838806;	Ogilvie D.J., Ye		loning and mappin	ESTs including 3 members of the Cystatin gene family and	ion of CpG island	Genomics 32:425-430(1996).	EMBL; X88976; CAA61407.1;	8	8 AA; 925 MW; FD5411A7376871E6 CRC64;		Query Match 81.8%; Best Local Similarity 66.7%;	2; Conservative
LT 1 58	016468	016468;	01-NOV-1996	01-MAY-1999	01-DEC-2001	DNA for cost	Homo sapiens (Human).	Eukaryota; 1	Mammalia; E	NCBI TaxID=9606;	_ [T]	SEQUENCE FROM N.A.	MEDLINE=964	James L.A.,	Anand R.;	"Walking, cl	ESTs includi	identificati	Genomics 32:	EMBL; X88976	NON TER	SEOUENCE		ery Match st Local Simi	Matches 2;
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B AA. RESULT 2
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   NCBI_TaxID=36310;
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Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
"Conserved tRNA gene cluster in starfish mitochondrial DNA.";
Curr. Genet. 15:193-206(1989).
EMBL; X16886; CAA34767.1; -.
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Boldorini R., Caldarelli-Stefano R., Monga G., Zocchi M., Mediati M.,
Tosoni A., Ferrante P.;
"PCR detection of JC virus DNA in the brain tissue of a 9-year-old
child with pleomorphic xanthoastrocytoma.";
J. Neurovirol. 4:242-245[198].
EMBL; AF064547; AAC23995.1;
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Mitochondrion.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
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                                                   COI gene product (Fragment).
Asterina pectinifera (Starfish).
Mitochondrion.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
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Gust Local Similarity 66.70,
Best Local Similarity 51.70,
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Polyomavirus JC.
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Lepidosauria, Squamata, Scleroglossa, Anguimorpha, Varanidae, Varanus.
NCBI_TaxID=62046;
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Lepidosauria, Squamata, Scleroglossa, Anguimorpha, Varanidae, Varanus.
NCBI_TaxID=169841;
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"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
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MEDLINE=99343618; PubMed=10413626; Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.; Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.; "Vicariant patterns of fragmentation among gekkonid lizards of the genus teratoscincus produced by the indian collision: A molecular phylogenetic perspective and an area cladogram for central asia."; Mol. Phylogenet. Evol. 12:320-332(1999).
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SEQÜENCE 9 AA; 1188 MW; 428CB9C9D36411A7 CRC64;
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66.7%;
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Similarity 66.7%;
2; Conservative
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EMBL; AF407500; AAL10054.1;
Mitochondrion.
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Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                   1 LXR 3
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01-DEC-2001
01-DEC-2001
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
NCBI_TaxID=169838;
    "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)."; Cladistics 17:0-0(2001).
Embi, AF407514; AAL10096.1; -Mitochondrion.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
NCBI_TaxID=62048;
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"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
Cladistics 17:0-0(2001).
EMBL; AF407518; AAL10108.1; -.
Mitochondrion.
                                                                                                                                                                                 Gaps
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Pred. No. 8.3e+05;
0; Mismatches 1; Indel
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Pred. No. 8.3e+05;
                                                                                                    9E80C7336411A731 CRC64;
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Last annotation update)
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotatio
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                      81.8%;
llarity 66.7%;
Conservative (
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66.7%;
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EMBL; AF407495; AAL10040.1;
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                                                                                 NON TER 9 9 9 SEQUENCE 9 AA; 1154 MW;
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9 AA; 1124 MW;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
2, Conserve
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SEQUENCE
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
NCBI_TaxID=62044;
                                        Gaps
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MEDLINE=87061221; PubMed=3023684;
MEDLINE=87061221; PubMed=3023684;
CLUKE W.F., Walker D.L., Peitzman L.B., Frisque R.J.;
"Construction and characterization of hybrid polyomavirus genomes.";
J. Virol. 60:960-971(1986)
EMBL; M14452; AAA96236.1; -.
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NCBI_TaxID=46771;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2001 (TrEMBLrel. 19, Last annotation update)
Papovavirus BK (Gardner derived clone BKV9) early transcription control region (Fragment).
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Length 9;
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Last sequence update)
Last annotation update)
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  DB 8; Le
8.3e+05;
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8.3e+05;
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Pred. No. 8.3e+
0; Mismatches
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                                      0; Mismatches
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  Score 9;
Pred. No.
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81.8%;
66.7%;
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66.7%;
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EMBL; AF407512; AAL10090.1;
Mitochondrion.
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                                    2; Conservative
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
NCBI_TaxID=169854;
                                                                                                                                                                                                                                                                           "Molecular phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families.";
Mol. Phylogenet. Evol. 12:250-272(1999).
EMBL, AF085608; AAD51514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ast J.C.; mitochondrial DNA evidence and evolution in Varanoidea (Squamata)."; Cladistics 17:0-0(2001). EMBL, AF407530; AAL10142.1; -. Mitochondrion.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae;
                                                                                                                                                                                                                         MEDLINE-99343613; PubMed-10413621;
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
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Pred. No. 3.8e+03;
0; Mismatches 1; Indels
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NON TER 10 10

SEQUENCE 10 AA; 1255 MW; 5DEE80C7336411A7 CRC64;
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SEQUENCE 10 Aa; 1255 MW; 5DEEB0C7336411A7 CRC64;
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
1-WAY-2000 (TrEMBLrel. 13, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                   Diploglossus bilobatus.
Mitochondrion.
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"Construction and characterization of hybrid polyomavirus genomes.";
J. Virol. 60:960-971(1986)
EMBL; M14451; AAA96235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21184280; PubMed=11286498; Macey J.R., Strasburg J.L., Brisson J.A., Vredenburg V.T., Jennings M., Larson A.; Molecular Phylogenetics of Western North American Frogs of the Rana boylli Species Group.", Mol. Phylogenet. Evol. 19:131-143(2001).
                                                                                                                                                                            Simiān virus 12.
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
VCBI_TaxID=46771;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=160499;
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                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Papovavirus BK (Gardner) early transcription control region
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10 AA; 1320 MW; 42D380C9D36411A7 CRC64;
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Witochlondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
                                                                                                   [1] — SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Agt J.C.; "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)."; Cladistics 17:0-0(2001).

EMBL, AR407515; AAL10099.1; -.

Mitochondrion.

NON TER 10 10 10

SEQUENCE 10 AA; 1234 MW; 584C4CA5A36411A7 CRC64;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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18 AA; 2173 MW; 61DABDFE4E317B0A CRC64;
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Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated genome analysis program.";
Theor. Appl. Genet. 93:99'-1005(1996).
-- MISCELLAMBOUS: OW THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, ITS MM IS: 31.6 kDa.
Maize-2DPAGE; P80631; COLEOPTILE.
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"Purification and N-terminal sequencing of a 3 kDa antibacterial peptide from skin secretions of rainbow trout.";
Submitted (MAY-2002) to the SWISS-PROT data bank.
-!- FUNCTION: Has antibacterial activity against Gram-positive bacterium P.citreus.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003795; F:antimicrobial peptide activity; NAS.
Antibiotic.
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01-MAR.1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
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nes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Coleoptile;
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                                                                                                                                                                                                                                                                                                                                                                                                                                LAR 14
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1D 18P4 PIG

AC P24854;

DT 01-MAR-199

DT 28-FEB-200

DE Insulin-lib

DE (IGF-bindlib

DE (IGF-bindlib
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UC25_MAIZE
UC25_MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                              "Anaerobic growth of Rhodopseudomonas palustris on 4-hydroxybenzoate is dependent on AadR, a member of the cyclic AMP receptor protein family of transcriptional regulators.";
J. Bacteriol. 174:5803-5813(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dispensa M., Thomas C.T., Kim M.K., Perrotta J.A., Gibson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9; DB 1; Length 16; Pred. No. 5.8e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40988840096655E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-C7T-2001 (Rel. 40, Last annotation update)
Hypothetical protein in aadR S'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA; 1799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M92426; AAA26089.1; -. PIR; A43334. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 81.8%;
Similarity 66.7%;
2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                NCBI_TaxID=9823;
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Fragment).
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P50475;
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SO CCC CCC CCC CCC STATA STATA
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-I- FUNCTION: Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocytemacrophage system and enhance the activity of immunoagents.

-I- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between Nacetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- MISCELLANBOUS: Lysozyme C is capable of both hydrolysis and transglycosylation; it shows also a slight esterase activity. It acts rapidly on both peptide-substituted and unsubstituted peptidoglycan, and slowly on chitin oligosaccharides.
-i- SIMILARITY: Belongs to family 22 of glycosyl hydrolases. PIR; A60525; A60525.
                                                                                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=M11k;
MEDLINE=90263403; PubMed=2344734;
Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.;
"Feline whey proteins: identification, isolation and initial characterization of alpha-lactalbumin, beta-lactoglobulin and
          Score 9; DB 1; Length 18;
Pred. No. 6.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9; DB 1; Length 20;
Pred. No. 7.3e+02;
0; Mismatches 1; Indels
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PROSITE; PS00128; LACTALBUMIN_LYSOZYME; PARTIAL.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                               20 AA.
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01-0CT-1994 (Rel. 30, Last seq
28-FEB-2003 (Rel. 41, Last ann
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             81.8%;
66.7%;
                                                      Conservative
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                                Similarity 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9685;
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P37863;
                                                                                                                                                                                                                                           LYC_FELCA
P37155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lysozyme."
        Query Match
Best Local S
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Matches
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthals.
-!- SIMILARITY: BESON STRNA SYNT Ala.
--- PROSITE; PS50860; AA TRNA LIGASE II ALA; PARTIAL.
--- Aminoacyl-tRNA synthētase; ProteIn biosynthesis; Ligase; ATP-binding.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94218258; PubMed=8165147; de Mot R., Schoofs G., Vanderleyden J.; "A putative regulatory gene downstream of recA is conserved in gramnegative and Gram-positive bacteria.";
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1-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
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0
                                                                                                                                                             Venkatesh T.V., Das H.K.;
"The Azotobacter vinelandii recA gene: sequence analysis and
regulation of expression.";
Gene 113:47-53(1992).
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Eur. J. Bacchem. 1981:201-210(1991).

-!- CATALYTIC ACTIVITY: ATP + L.-alanine + tRNA(Ala) = AMP

diphosphate + L.-alanyl-tRNA(Ala).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 22:1313-1314(1994).
-!- PUNCTION: Modulates recA activity (By similarity).
-!- SUBCELLULA LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE RECX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C809F8BCCED6CB56 CRC64;
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7.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9; DB 1;
Pred. No. 7.3e+
0; Mismatches
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                                                                                            SEQUENCE FROM N.A.
MEDLINE=92225347; PubMed=1563632;
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Pseudomonadaceae; Azotobacter.
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66.7%;
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Matches 2; Conservative
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                                  NCBI_TaxID=354;
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                                                                                                                                                                                                                                                                                                                               IDENTIFICATION
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J. Biochem. 104:917-923(1988).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
"Glutamine synthetase from a cyanobacterium, Phormidium lapideum:
purification, characterization, and comparison with other
cyanobacterial enzymes.";
                                                                                                                                              L-glutamine.
                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                PIR; PX0011; PX0011.
InterPro; IPR001691; GLN synth.
PROSITE; PS00180; GLNA_1; PARTIAL.
PROSITE; PS00181; GLNA_ATP; PARTIAL.
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Best Local Similarity
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les 2; Conserv
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P20056;
01-FEB-1991 (
01-FEB-1991 (
28-FEB-2003 (
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P80898;
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SEQUENCE
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NEUU_RANTE
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 174:142-148(1991).
-1- FUNCTION: VASORELAXANT ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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Sawa Y., Ochiai H., Yoshida K., Tanizawa K., Tanaka H., Soda K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arimura J.J., Minamino N., Kangawa K., Matsuo H.; "Isolation and identification of C-type natriuretic peptide in chicken brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; DB 1; Length 22;
Pred. No. 8.1e+02;
0; Mismatches 1; Indels
                                                                                                             81.8%; Score 9; DB 1; Length 21; llarity 66.7%; Pred. No. 7.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Oscillatoriales; Phormidium.
NCBI_TaxID=32060;
  1 1
21 21
21 AA; 2293 MW; D739DDC62CD43375 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 22
22 AA; 2244 MW; FC2A4706D8DAC025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
10-MAY-1991 (Rel. 18, Last sequence update)
10-CTZ-2001 (Rel. 40, Last annotation update)
C-type natriuretic peptide (CNP).
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Pfam; PF00212; ANP; 1.
SMO010; NATPEPTIDES.
SMART; SM00183; NAT PEP; 1.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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66.7%;
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Best Local Similarity 66.7°
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Phormidium lapideum.
                                                                                                                                        Local Similarity
nes 2; Conserv
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NCBI_TaxID=9031;
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P20479;
NON_TER
NON_TER
SEQUENCE
                                                                                                                Query Match
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GLNA PHOLP
                                                                                                                                                                        Matches
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-- FUNCTION: Hydrolyzes PPi generated in anabolic reactions.
-- CATALYTIC ACTIVITY: Diphosphate + H(2)0 = 2 phosphate.
-- COPACTOR: Requires the presence of divalent metal cation.
Magnesium confers the highest activity. Binds 4 divalent cations per submit (By similarity).
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                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 1; Length 25;
Pred. No. 9.3e+02;
0; Mismatches 1; Indels
                                                         81.8%; Score 9; DB 1; Length 23; ilarity 66.7%; Pred. No. 8.5e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudanabaena sp. (strain PCC 6901).
Bacteria; Cyanobacteria; Oscillatoriales; Pseudanabaena.
NCBI_TaxID=47918;
23 23 AA; 2656 MW; 20B69C164D2A5739 CRC64;
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(Rel. 17, Last sequence update)
(Rel. 41, Last annotation update)
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Similarity 66.7%;
2; Conservative
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Query Match
Best Local Similarity
Matches 2; Conserv
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01-NOV-1995
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P41502;
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                                                                                                                                                 TISSUE=Intestine;

X MEDLINE=90078173; PubMed=2592357;

A Domin J., Yiangou Y.G., Spokes R.A., Aitken A., Parmar K.B.,
Chrysanthou B.J., Bloom S.R.;
T "The distribution, purification, and pharmacological action of an amphibian neuromedin U.";
T amphibian neuromedin U.";
J. Blol. Chem. 264:20881-20885 [1989].
-!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES SELECTIVE VASCONORISTICTION.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE NMU FAMILY.
R PIR, 344179; A44179.
R InterPro; IPR001942; NMU.
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J. Biol. 10nem. 276:4085-4092 (2001).
J. Biol. Chem. 276:4085-4092 (2001).
C.-I. FUNCTION: ACTIVE AGAINST GRAM-POSITIVE BACTERIA B.WEGATERIUM AND M.LUTEUS, GRAM-NEGATIVE BACTERIA B.COLI SBS363 AND D22,
K.PNEUMONIAE, S.TYPHIMURIUM AND P.ARRUGINOSA, YEAST C.ALBICANS AND FILAMENTOUS FUNGI F.CULMORUM, N.CRASSA, N.HEMATOCOCCA AND T.VIRIDAE. INACTIVE AGAINST GRAM-POSITIVE BACTERIA B.SUBTILIS, S.PYOGENES, B.THURINGIENIST AND S.AUREUS, GRAM-NEGATIVE BACTERIA B.C.CLOACAE AND E.CAROTOVORA AND FILAMENTOUS FUNGUS B.BASSIANA.
C.-I. INDUCTION: By bacterial infection.
C.-I. MASS SPECTROMETRY: WW=3001.8; METHOD=WALDI.
C.-I. MASS SPECTROMETRY: WW=3001.8; METHOD=WALDI.
MALIDIOLIC; FUNGICIGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    Rana temporaria (European common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, MASS SPECTROMETRY, AND FUNCTION.
TISSUE-B1006, and Salivary gland;
PubMed-11053427;
Lamberty M., Zachary D., Lanot R., Bordereau C., Robert A.,
Hoffmann J.A., Bulet P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 9; DB 1; Length 25;
Pred. No. 9.3e+02;
0; Mismatches 1; Indels
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MISSING (IN C-4 ISOFORM).
AA79370264262F60 CRC64;
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6A01D89F6DA06FD4 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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25 AA; 3001 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00084; NMU; 1.
PROSITE; PS00967; NMU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 2; Conservative
  Neuromedin U-25 (NmU-25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amidation; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=115113;
                                                                                   NCBI_TaxID=8407;
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Antonioli S., Banchi N., Cecarelli P., Pula G., Sorci G.,
Antonioli S., Bocchini V., Donato R.;
"Neuron-specific" protein gene product 9.5 (PGP 9.5) is also
"Neuron-specific" protein gene product 9.5 (PGP 9.5) is also
"T expressed in giloma cell lines and its expression depends on cellular
"T growth state.";
"I FEBS Lett. 290:131-134(1991).
"THIS BELL 200:131-134(1991).
"THIS BENTAME IS A THIOL PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINS.
THIS BYTAME IS A THICL PROTEIN CLEATING OF UBIQUITIN.

-I CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
"Diquitin + a thiol."

-I SUBCELLULAR LOCATION: Cytoplasmic.
-I SUBCELLULAR LOCATION: Cytoplasmic.
-I TISSUE SPECIFICITY: NEURONS AND CELLS OF THE DIFFUSE
NEUROSING TO PEPTIDASE FAMILY C12.

PIR, 517561; S17561.

PROCESSING TO PEPTIDASE FAMILY C12.

PROCESSING TO PEPTIDASE FAMILY C12.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR001578; UCH 1.
Pfam; PF010B8; Peptidase_C12; 1.
PF03TE; PS00140; UCH 1; PARTIAL.
Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
NON_TER 25 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase isozyme Ll (EC 3.4.19.12) (11) (Ubiquitin thiolesterase Ll) (Neuron cytoplasmic protein 9.5) (PGP 9.5) (PGP9.5) (Fragment).
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Length 25;
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Nitrogen assimilation regulatory protein (Fragment).
DB 1; Le
9.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 9; DB 1; Loge. 7%; Pred. No. 9.3e+02;
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 AA
                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Rhizobium leguminosarum (biovar phaseoli)
   Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92008646; PubMed=1833240;
81.8%;
                                                           2; Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
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CR Thirobiaceae; Rhizobian/Agrobacteria; Rhizobiane;
CR Thirobiaceae; Rhizobian/Agrobacteriam group; Rhizobian.
CR Thirobiaceae; Rhizobian/Agrobacterium group; Rhizobian.
CR TRAID=383;
CR TRAIN=281.
CR TRAID=381.
CR TRAID=382.
CR TR THE ACTOR A., Tate R., Colonna-Romano S., Iaccarino M., Defez R., Riccio A., Tate R., Colonna-Romano S., Iaccarino M., Defez R., The ntrEC genes of Rhizobian leguminosarum are part of a complex operno subject to negative segulation.";
CR TR TR TR TRAIDENCY CONSTRUCTON: NUMBER OF THE TWO-COMPONENT RECULATORY CENES SUCH AS CRIM. M. MITCODIOL. 9:669-577(1991).
CC GLIMA. WITE ACTIVATION OF NUTROCEN ASSIMILATORY CENES SUCH AS CRIM. M. MITCODIOL. 9:669-577(1991).
CC GLIMA. WITE ACTIVATION OF NUTROCEN ASSIMILATORY CENES SUCH AS CRIM. ASSIMILATORY CENES SUCH AS CRIM. M. THE ACTIVATION OF SUCH ASSIMILATORY CENES SUCH AS CRIM. M. MITCOPACH ASSIMILATORY CENES SUCH ASSIMILATORY CENES SUCH
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Search completed: December 8, 2003, 09:14:15 Job time : 2.05051 secs

1 LXR 3 | | | 22 LSR 24

8 6

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 8, 2003, 09:13:30; Search time 1.65657 Seconds (without alignments) 232.212 Million cell updates/sec Run on:

US-09-498-556C-357

1 LXRX 4 Title: . Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Query Match	å Query Match Length	DB	αI	Description
-	6	81.8	7	~	E48394	alveoprotein compo
7	6	81.8		7	B48394	О
m	σ	81.8	80	0	PC4131	hypothetical prote
4	σ	81.8	œ	(7)	T13818	×
S	o,	81.8	. 10	0	T13838	cytochrome-c oxida
9	σ	81.8	10	7	T14219	
7	đ	81.8	11	N	PU0034	
89	σ	81.8	12	~	A42324	\sim
σ	σ	81.8	13	7	PT0293	Ig heavy chain CRD
10	σ	;	14	~	PA0111	protein QA100054 -
11	σ	81.8	15	7	836896	ribosomal protein
12	6	81.8	15	7	PA0075	fructose-bisphosph
13	6		15	~	PA0102	fructose-bisphosph
14	σ	81.8	15	~	B32800	hypothetical prote
15	σ	81.8	15	~	PH1455	T-cell receptor al
16	Q	81.8	15.	~	AF0832	phe leader peptide
17	o,	ä	16	~	C61414	chymotrypsin (EC 3
18	Ø.	ä	16	N	JH0517	insulin-like growt
19	σ	81.8	16	~	B44036	collagen alpha 1(X
50	σ	81.8	17	~	JP0046	ribosomal protein
21	σ	-	17	~	A34835	ribosomal protein
22	0	;	17	7	I54269	vitamin D binding
23	0	Ξ.	17	7	JQ2310	hypothetical 2.1K
24	6	81.8	17	~	JQ2320	hypothetical 2.1K
25	σ	ä	17	~	B61414	chymotrypsin (EC 3
56	σ	Ή.	18	0	S29491	GTP-binding protei
27	σ	Η.	18	~	A41877	
28	o	81.8	18	7	A43334	adk -
29	O	81.8	18	7	S33645	hypothetical prote

hypothetical prote	glycogen(starch) s	homeobox 5 protein	cholecystokinin-58	lysozyme (EC 3.2.1	ribosomal protein	ribosomal protein	hypothetical prote	serine proteinase	globin - polychaet	chymotrypsin (EC 3	J-kappa recombinat	probable trp opero	alanine-tRNA ligas	natriuretic peptid	insulin-like growt
S10452	S02269	JC2060	A60326	A60525	JP0050	JP0051	533001	PC2084	819616	A61414	A42267	AC0269	S16073	JT0581	F23734
7	~	~	~	ď	0	7	~	N	~	N	~	~	~	7	7
18	19	19	19	20	20	20	20	20	20	20	20	50	21	22	22
81.8	81.8	81,8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8
0	σ	σ	σ	σ	σ	0	Φ	ģ,	σ	σ	σ	σ	σ	σ	σ
30	31	32	33	34 .	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr. C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: E48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: sequence extracted from NCBI backbone (NCBIP:131450) C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                             A; Reference number: A48394; MUID: 93250576; PMID: 8485470
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAT>
A;Experimental source: milk
                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: E48394
                                                                                                                                                                                                                                                                                                         II-like sequences.
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Score 9; DB 2; Length 7; Pred. No. 2.8e+05; 0; Mismatches 1; Indel Query Match Best Local Similarity 66.7%;

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Gaps

. 0

1; Indels 2; Conservative 1 LXR 3 5 LAR 7 Matches ò g

C;Species: Cavia porcellus (guinea pig) C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995 C;Accession: B48394 major fat-globule membrane protein GP 55 - guinea pig (fragment)

R;Mather, I.H.; Banghart, L.R.; Lane, W.S. Biochem. Mol. Biol. Int. 29, 545-554, 1993 A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

A;Reference number: A48394; MUID:93250576; PMID:8485470 A;Accession: B48394

A; Status: preliminary A; Molecule type: protein

A;Experimental source: milk A;Note: sequence extracted from NCBI backbone (NCBIP:131444)

Gaps ö 1; Indels Length 7; Query Match 81.8%; Score 9; DB 2; Le Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 1.

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A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase
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C;Species: Rattus norvegicus (Norway rat)
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Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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A; Accession: PU0034
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Les 2; Conserv
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Matches
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C;Species: mitochondrion Bipes biporus
C;Species: mitochondrion Bipes biporus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13838
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T13838
A;Accession: T13838
A;Accession: T13838
A;Accession: Date orders and the role of light-strand replication in rearrangement A;Accession: T13838
A;Accession: T13838
A;Accession: T13838
A;Reference number: DAA
A;Residues: 1-10 cMAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cycochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
Cybecies: mitochondrion Myxine glutinosa (Atlantic hagfish)
Cybecies: O-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
CyAccession: T13818
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mylitle: The main features of the craniate mitochondrial DNA between the ND1 and the COI A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13818
A;A
                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme dl.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-8 <KAW-
A,Cross-references: DDBJ:DS0473; NID:g1217594
A,Cross-references: DDBJ:DS0473; NID:g1217594
A,Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                  nypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
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Best Local Similarity 66.7°
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A, Note: COI
C, Keywords: mitochondrion
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Cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment) C;Species: mitochondrion Xenosaurus grandis C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T14219
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T14219
A;Macey, J.R.; Latson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T14219
A;Accession: T14219
A;Accession: T14219
A;Accession: T14210
A;Access
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V:Vezono, Y.; Tsumori, H.; Mukasa, H.
submitted to JIPID, October 1993
A;Description: Purification and properties of glucosyltransferase synthesizing 1,6-alpha-
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A;Cross-references: EMBL:U71335; NID:g1753232; PID:g1753235; PIDN:AAB48271.1
C;Genetics:
A;Geneme: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase
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C;Species: Streptococcus bovis
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996
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Pred. No. 1.1e+03;
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A;Residues: 1-114 (1822>
A;Experimental source: ATCC 9809
C;Keywords: glycosyltransferase; hexosyltransferase
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Cipate: 13-dan-1995 Harmine Ervision 13-dan-1995 #text_change 13-Jan-1995 Cipate: 13-dan-1995 Gipate: 13-dan-1995 Harmine Side Gipate: 13-dan-1995 Gipate: 13-dan-1995 Gipate: 13-dan-1995 Gipate: 13-dan-1995 Gipate: 13-dan-1995 Higher Side Gipate: 13-dan-
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A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotric?
A;Reference number: PA0051
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A; Residues: 1-15 <CRO>
A; Residues: 1-15 <CRO>
A; Accession: PA0077
A; Molecule type: protein
A; Residues: 1-15 <CRO>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0102
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Pred. No. 1.7e+03;
0; Mismatches 1;
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A,Residues: 1-15 <CHO>
C,Keywords: aldehyde-lyase; carbon-carbon lyase
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Best Local Similarity 66.7%;
Matches 2; Conservative
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C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Feb-1996
C;Accession: A42234
R;Shayiq, R.M.; Avadhani, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitod
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C;Species: Homo sapiens (man)
C;Accession: PT0293
R;Yamada, M: Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0293
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-13 <YAM>A;Residues: 1-13 <YAM>A;Residues: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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CiDate: 07-ppr-1995 #sequence_revision 26-May-1995 #text_change 06-Jun-1997
CiAccession: PA0111
R;Kamo, M.; Kawakami, T.; Tsugita, A.
B;Kamo, M.; Kawakami, T.; Tsugita, A.
B;Reference number: PA0109
A;Reference number: PA0109
A;Reference pa0111
A;Reference number: PA0101
A;Reference number: PA0109
A;Reference number: PA0109
A;Reference number: PA0109
A;Reference number: PA0109
A;Reference number: PAMA>
A;Reference number: PAMA>
A;Refidues: 1-14 < KAM>
A;Re
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <SHA>
A;Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIP:78410)
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836896
ribosomal protein S16 - Mycobacterium bovis (fragment)
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Best Local Similarity 66.7%;
Matches 2; Conservative
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T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Accession: PH1455
B;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; KC
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUD:93171821; PMID:8436911
A;Reference number: PH1430; MUD:93171821; PMID:8436911
A;Residues: 1-15 - CAS>
A;Residues: 1-15 - CAS>
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
                                                                                                    B32800

Hypothetical protein (Pl 5' region) - human (fragment)

Cippedies: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993

Ciptedies: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993

Ciptedies: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993

Ciptedies: Dadani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.

Mol. Cell. Balol, 9, 2279-2283, 1989

A.Title: Primary structure of a human mitochondrial protein homologous to the bacterial A.Aceference number: A32800; MUID:89313783; PMID:2568584

A.Status: preliminary

A.Status: preliminary

A.Status: Lype: mRNA

A.Reseidues: alls

A.Status: A32800
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels
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81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 66.7
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